Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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- protein search, using sw model OM protein

September 22, 2005, 14:39:13 Run on:

3 ; Search time 169 Seconds (without alignments) 1375.402 Million cell updates/sec

US-10-712-479-2

3167 1 MASMSYTWTGALITPCAA......LLSVGVGIYLLPNRHHHHHH 601 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:*
geneseqp1990s:*
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geneseqp2001s:* A_Geneseq_16Dec04:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ado19021 Full-lend	Ado19023 C-termina		Aaw01679 NS5B prot	Aaw01680 HCV NS2-N	Aar20111 Non-A, no	Aar20091 Non-A, no	Adf88597 Hepatitis	Aaw98022 Infection	Aab31170 Amino aci	Ado36227 Hepatitis	Ado79401 Hepatitis	Ado36215 Hepatitis	Ado79389 Hepatitis	Aay06423 Non-A, no	Aar68864 Hepatitis	Aab60130 Hepatitis	Aao26416 Protein d	Abu09575 HCV Met-N	Aar68622 HCV prote	Aag79560 HCV NS5B		Aae18903 Hepatitis	Abp71699 HCV NS5B	Abr41892 Hepatitis
	ID	ADO19021	ADO19023	AAR30616	AAW01679	AAW01680	AAR20111	AAR20091	ADF88597	AAW98022	AAB31170	AD036227	AD079401	AD036215	AD079389	AAY06423	AAR68864	AAB60130	AA026416	ABU09575	AAR68622	AAG79560	AAG79556	AAE18903	ABP71699	ABR41892
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de	Query Match	100.0	95.8	92.6	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1
	Score	3167	3034.5	3027	3016	3016	3016	3016	3016	3015	3015	3015	3015	3014	3014	3014	3013	3012	3012	3012	3012	3011	3011	3011	3011	3011
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ABP97967 AAG79561 ADG19078	AAR82694 AA018001 AAE15729	AAE15731 AAE15720 AAE15717	AAE15727 AAE15728 AAE15722	ABC 30591 ABC 30591 ABC 30600	ABG30581 ABG30586 ABG30593 ABG30582
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ALIGNMENTS

Detecting RNA polymerase activity in a continuous-read manner, useful in treating osteoporosis, carcinomas, cardiovascular diseases, ocular disorders or arthritis, by contacting an RNA polymerase with an oligonucleotide template. Heparitis C virus infection, HCV infection; polymerase; NS5B; bone mineral disease; osteoporosis; carcinoma; cardiovascular disease; diabetes; ocular disorder; renal dysfunction; lymphoma; lymphoproliferative disorder; metabolic disorder; arthritis; sleep disorder; thyroid disorder; antiinflammatory; hepatotropic; virucide; osteopathic; cycostatic, antiinflammatory; hepatotropic; ortopic; antiatic; enzyme. Sheets MP, Wells PA, Shelly JA, Poorman RA, Epps DE; polymerase activity; continuous-read assay; Full-length HCV NS5B polymerase, FL NS5B. Ź AD019021 standard; protein; 601 13-NOV-2003; 2003WO-US036465. 13-NOV-2002; 2002US-0425981P. (first entry) WPI; 2004-420337/39. (PFIZ) PFIZER INC. Hepatitis C virus WO2004044228-A2. N-PSDB; ADO19020 27-MAY-2004. 12-AUG-2004 Morgan AG; AD019021; Yagi Y, RESULT 1 ADO1902

Claim 5; SEQ ID NO 2; 46pp; English.

The present invention relates to a method for detecting RNA polymerase estivity in a continuous-read manner. The method comprises contacting an RNA polymerase with an oligonucleotide template in a reaction mixture comprising an assay buffer, under conditions in which the RNA polymerase

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is active, adding a fluorescent dye capable of binding double-stranded nucleic acid molecules to the reaction mixture, and measuring the fluorescence of the reaction mixture. The RNA polymerase is the Hepatitis C virus (HCV) polymerase, NSSB. The method is useful for treating HCV infection, bone mineral diseases like osteoporosis, carcinomas, acatiovascular diseases, diabetes, ocular disorders, renal dysfunction, lymphomas, lymphoproliferative disorders, metabolic disorders, arthritis, sleep disorders and thyroid disorders. The present sequence represents full-length HCV NSSB polymerase (designated FL NSSB).
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Hepatitis C virus infection; HCV infection; polymerase; NS5B;
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The present invention relates to a method for detecting RNA polymerase activity in a continuous-read manner. The method comprises contacting an RNA polymerase with an oligonucleotide template in a reaction mixture comprising an assay buffer, under conditions in which the RNA polymerase is active, adding a fluorescent dye capable of binding double-stranded nucleic acid molecules to the reaction mixture, and measuring the fluorescence of the reaction mixture. The RNA polymerase is the Hepatitis C virus (HCV) polymerase, NSSB. The method is useful for treating HCV infection, bone mineral diseases like osteoporosis, carcinomas, cardiovascular diseases, diabetes, ocular disorders, renal dysfunction, lymphomas, lymphopoliferative disorders, metabolic disorders, arthritis, sleep disorders and thyroid disorders. The present sequence represents C terminally truncated HCV NSSB polymerase (designated Cdeltazl NSSB).
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bone mineral disease; osteoporosis; carcinoma, cardiovascular dise
diabetes; ocular disorder; renal dysfunction; lymphoma;
lymphoproliferative disorder; metabolic disorder; arthritis;
sleep disorder; thyroid disorder; antinflammatory; hepatotropic;
virucide; osteopathic; cytostatic; antidiabetic; ophthalmological;
nephrotropic; antiarthritic; enzyme.
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Matches 580; Conservative
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                                                                                                                                     Hepatitis C virus
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95.6%; Score 3027; DB 2; 96.8%; Pred. No. 1.3e-279; tive 9; Mismatches 10;
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(revised)
(first entry)
                                            Best Local Similarity 96.8
Matches 572; Conservative
     Sequence 3010 AA
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25-MAR-2003
19-AUG-1997
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                                                                                                                                                                                                             TPIPAASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNRHHHHH 600
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EYDLELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYA
                                                                                                                                                                                                                            PTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHS
                                                                                                                YSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKL
                                                                                                                                                                      EYDLELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide coded by Korean HCV full cDNA sequence LBC1
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                                                                                                                                                                                                                                                                                                                                                                  AAR30616 standard; protein; 3010 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHCV-LBC1; diagnosis; vaccine
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N-PSDB; AAQ33282.
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Yang JY;
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19-MAY-1993
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Kim ST,
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                                                                                2420 SMSYTWIGALITPCAAEESKLPINPLSNSLLRHINMVYATISRSAGLRQKKVTFDRLQVL
                                                                                                                                                                                                                                                           DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2780 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAMETARHTPVNSWLGNIIMYAPTLW
                                                  5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
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Gaps
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Indels
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RRARD) activity or the terminal molectidy! transferase (RMESE) activity encoded by hepatitis C virus (HCV), is characterised in that sequences concerned by hepatitis C virus (HCV), is characterised in that sequences concerned by hepatitis C virus (HCV), is characterised in that sequences content of the activities of RARD and TYMESE encoded by HCV in order to vitro the activities of RARD and TYMESE compounds that inhibit these carymatic activities and therefore might interfere with the replication of the HCV. The present sequence comprises amino acids 2420-3010 of the HCV DOLYprotein and corresponds to the NSSB protein. cDNA encoding this protein was cloned between the BamHI and HindIII sites of pBlueBacIII to form pBacSB. Another expression plasmid, pBacSC (containing cDNA encoding amino acids 810-3010 of HCV; see AAMO1680) was also constructed. Extracts of BacSS- or BacSB-infected Sf9 cells contain a novel magnesium-dependent content and corresponds to the input RNA molecule. As the products was shown to be dependent on the presence of RNA, but independent of an added primer or of the origin of the input RNA molecule. As the products cappeared to be identical, the experiments indicated that the observed RARD activity is encoded by the HCV NSSB protein. (Updated on 25-MAR-2003 CCC to correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDHYRDVLKEMKAKASTVKAKLLSVEEACKITPPHSAKSKFGYGAKDVRNLSSKAVNHIH 120
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                                                                                                                                     Reproducing enzymatic activities of HCV in vitro - using sequences contg.
NS5B for RNA-dependent RNA polymerase and terminal nucleotidyl
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                                                                                                                                                                                                                                                                              A novel method for reproducing in vitro the RNA-dependent RNA polymerase
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95.2%; Score 3016; DB 2; Length 591;
Best Local Similarity 96.6%; Pred. No. 1.2e-279;
Matches 571; Conservative 11; Mismatches 9; Indels (
(RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                           De Francesco R, Tomei L, Behrens S;
                                                                                                                                                                                                                                  Claim 1; Page 24-26; 49pp; English
                                                                                                                                                                                      transferase activities.
                                                                                            WPI; 1997-021225/02.
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Radrago activity or the terminal nucleotidyl transferase (TNTase) activity or the terminal nucleotidyl transferase (TNTase) activity or the terminal nucleotidyl transferase (TNTase) activity or concernoded by hospatitis C virus (HCV), is characterised in that sequences concernoded by NSSB are used in the mixture. The method is used for assaying in viro the activities of RdRp and TNTase encoded by HCV in order to clentify, for therapeutic purposes, compounds that inhibit these enzymatic activities and therefore might interfere with the replication of the HCV. The present sequence comprises amino acids 810-3010 of the NC polyprotein and corresponds to NS2-NSSB procteins. CDNA encoding this protein mass cloned between the Ncol and HindIII sites of pBlueBacIII to form pBac25. Another expression plasmid, pBac5B (containing cDNA encoding amino acids 2420-3010 of HCV; see AAW01679) was also constructed.

Extracts of Bac25- or Bac5B-infected Sf9 cells contain a novel magnesium-dependent enzymatic activity that catalyses de novo RNA synthesis. This closendent of an added primer or of the presence of RNA, but condected a shown to be dependent on the presence of RNA, but condected that the observed RGRp activity is encoded by the HCV NSSB condected that the observed RGRp activity is encoded by the HCV NSSB protein. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 17-OCT 2003 to standardise OS field)
481 EINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWAVKTKLTPIP 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reproducing enzymatic activities of HCV in vitro - using sequences contg. NSSB for RNA-dependent RNA polymerase and terminal nucleotidyl transferase activities.
                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; non-structural protein; NS5B; polyprotein; RNA-dependent RNA polymerase; RdRp; terminal nucleotidyl transferase; TNTase; method; assay; in vitro activity; therapy; inhibitor.
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                                           545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
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                                                                                                                                                                                                                                                                                                                                                                         !CV NS2-NS5B non-structural protein.
                                                                                                                                                                                              AAW01680 standard; protein; 2201 AA
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WPI; 1992-009412/02.
N-PSDB; AAQ20268.
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28-DEC-1990;
08-MAY-1991;
14-MAY-1991;
                                                                           25-JUN-1991;
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31-AUG-1990;
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                                                                                                             1671 DDHYRDVLKEMKAKASTVKAKILSVEBACKITPPHSAKSKFGYGAKDVRNLSSKAVNHIH 1730
                                                                                          1791 TLPQVVMGSSYGFQYSPGQRVEFLVNTWKSKKNPMGFSYDTRCFDSTVTENDIRVEESIY 1850
                                                                                                                                                2031 ARMILMTHFPSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 2090
                                                                                                                                                                                                                                   DDHYRDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                  TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
                                                                                                                                         AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
                                                                                                                                                                     BLITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
                                                                                                                                                                                                ARMILMITHPFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                           EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP 544
                                                     SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLROKKVIFDRLQVL
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/label= NS2
11007. .1614
/label= NS3
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(first entry)
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non-B hepatitis virus.
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AACRAAKLODCTMLVNGDDLVVICESAGTOEDAASLRVFTEAMTRYSAPPGDPPOPEYDL 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2480 DDHYRDVLKEMKAKASTVKAKCLISVEBACKCITPPHSAKSKFGYGAKDVRNLSSKAVNHIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2540 SVWKDLLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-A, non-B hepatitis virus (NANBV) particles - as vaccines, immuno-
diagnostics and screening agents for NANBV, and to remove NANBV from
blood.
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1615, .1862
/label= NS4a
1863. .2012
/label= NS4b
2013. .3010
/label= NS5
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90JP-00230921.
90JP-00305605.
90US-00435451.
91JP-00138493.
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The sequence was deduced from several overlapping "BK" cDNA clones obtd. by "gene walking" using a cDNA clone isolated from a library prepd. from MANBAR NRA. Antigenic polypeptides from the sequence can be used as immunoassay reagents, for screening donated blood, and as immunogens for vaccine prodn. Antibodies raised to the peptides can be used in immunoassays to detect or quantify NANBV antigens in liver tissue and blood. Preferred polypeptides are include residues 1-30, -115, or 2012; 47-77; 116-191; 192-207 or -298; 230-218 or -263; 287-300; 293-330; 390-729; 730-1005; 1006-1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012; and 2013-3010. The sequence is also disclosed in EP-46348 (SEQ ID NO 1) in which a virus particle contg. antigens encoded by the sequence is claimed. See AAR20111 for details of this specification. (Updated on 25-MAR-2003 to correct PA field.)
New DNA from non-A, non-B hepatitis virus - and derived antigenic polypeptide(s) useful for diagnostics, blood screening and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2420 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNWYYATTSRSAGLRQKKVTFDRLQVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2660 QCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS
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                                                       Claim 3, Fig 2, 89pp; English
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                     424
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                                                                                                                                                                                        EINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWAVKTKLKLTPIP
                     ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLM
                                                                                            ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG
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/abel= C

/note= "core protein"

116. .191

/nabel= M

/note= "matrix protein"

192. .389

/abel= E

/note= "envelope protein"

390. .729

730. .1006

/label= NS1
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90JP-00305605.
91EP-00401604.
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/label= NS3
1615. .1862
/label= NS4a
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/label= NS4b
2013. .3010
/label= NS5
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(first entry)
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non-B hepatitis virus.
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N-PSDB; AAQ21829.
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01-MAY-1992
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2420 SMSYTWTGALITPCAAEESKLPINPLSNSLLRHHSMVYSTTSRSASLRQKKVTFDRLQVL 2479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2540 SVWEDLLEDTETPIDITIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2600 TLPQAVMGPSYGFQYSPGQRVEFLVNTWKSKKCPMGFSYDTRCFDSTVTENDIRTEESIY 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2660 QCCDLAPEARQAIRSLIERLYVGGPLINSKGQNCGYRRCRASGVLITSCGNTLTCYLKAT 2719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2780 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETVRHTPVNSWLGNIMYAPTLW 2839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 ARMILMTHFFSILLLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the novel testing method for diagnosing liver cancer. The novel method comprises amplifying the amino terminal region of a hepatitis-C virus NS3 gene using a predetermined primer and determining the hepatitis-C virus in a base sequence of the obtained DNA fragment. The novel testing method is useful for diagnosing liver cancer and also used in a gene amplification technique, a clinical laboratory test reagent, a polymerase chain reaction, a base sequence analysis and genetic engineering. The method enables the detection of a hepatitis-C virus having high carcinogenicity with high specificity. This sequence represents the protein of the hepatitis-C virus NS3 gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing liver cancer, involves amplifying amino terminal region of hepatitis-C virus gene using predetermined primer and determining hepatitis-C virus in base sequence of obtained DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVPPDLGVRVCEKMALYDVVS
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                                                          liver cancer; hepatitis-C virus; NS3 gene; carcinogenicity.
                   Hepatitis C virus NS3 gene protein, SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                           (SHIN-) ZH SHINSANGYO SOZO KENKYU KIKO.
                                                                                                                                                                                                                         30-MAY-2002; 2002JP-00158335.
                                                                                                                                                                                                                                                                  16-NOV-2001; 2001JP-00352443
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Best Local Similarity 96.3
Matches 569; Conservative
                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-819836/77
                                                                                                 Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADF88596
                                                                                                                                          JP2003210181-A
                                                                                                                                                                                29-JUL-2003
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genotype 1b strain HC-J4 groune (see AAX24833). HC-J4 was obtained from acute phase plasma of a chimpanzee infected with serum containing HC-J4/91. The infectious nucleic acid sequence can be used to produce chimperic genomes (see AAX24833) consisting of the open reading frames of infectious nucleic acid sequences of other genotypes (including genotypes (including genotypes (including plants)). The invention also relates to the introduction of mutations or deletions into infectious nucleic acid sequences in order to produce an attenuated that with suitable for vaccine development. Infectious nucleic acid sequences can also be used to produce attenuated virus uitable for vaccine development. Infectious nucleic acid sequences can also be used to produce attenuated virus uitable for without any of the viruses produced by transfection of a host cell vitro or in vivo of the viruses produced by transfection of a host cell configuration in the infectious nucleic acid sequence are used to immunise mammals, especially humans, against hepatitis C. The nucleic configuration acid sequences can also be used to induce protective immunity against the virus. The nucleic acid sequences or their encoded proteases (e.g. NS3 protease) can additionally be used to develop screening assays to identify antiviral agents for HCV
2840 ARMILATHFEILLAGEGLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 2899
                                                                 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV; infectious clone; infection; diagnosis; therapy; vaccine; screening; assay; antiviral; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV infections and for
                                                                                      2900 EINRVASCLEKTGVPPLEVWRHRARSVRAKTLSQGGRAATCGKYLFNWAVKTKLKTTPIP
                                                              485 EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP
                                                                                                                                                                  2960 AASQLDLSGWFVAGYNGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLDNR 3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein is encoded by the infectious hepatitis C virus (HCV)
                                                                                                                                                                                                                                                                                                                                                                                                                       Infectious hepatitis C virus genotype 1b strain HC-J4 protein.
                                                                                                                                               545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3015; DB 2; Length 3010;
Pred. No. 1.9e-278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                           AAW98022 standard; protein; 3010 AA
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98US-00014416.
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27-JAN-1998;
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ID AAWS
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2480 DDHYRDVLKEMKAKASTVKAKLLSIEEACKLTPPHSAKSKFGYGAKDVRNLSSRAVNHIR 2539
                                                                                                                                               2540 SVWEDLLEDTETPIDTTIMAKSEVFCYQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2599
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                                         2420 SMSYTWTGALITPCAAEESKLPINPLSNSLLRHHNMVYATTSRSASLRQKKVTFDRLQVL
                                                                               DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
                                                                                                                                                                                                        2600 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKSKKCPMGFSYDTRCFDSTVTESDIRVEESIY
                                                                                                                                                                                                                                                                                                                   2720 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAAALRAFTEAMTRYSAPPGDPPQPEYDL
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                                                                                                                                                                                         TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                                                                              QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA
                                                                                                                                                                                                                                                                                                    305 AACRAAKLODCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                                                                                                                                                                                                                                                                                                          ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLTPIP
                          SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a hepatitis C virus (HCV) clone genotype 1b.
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8; Indels
 16; Mismatches
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 567; Conservative
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N-PSDB; AAC86939.
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The specification describes a nucleic acid comprising a chimeric virus genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the fun-)structural region has been replaced by the fun-)structural region of a hepatitis C virus (HCV) genome. The nucleic acids comprising the chimeric virus and the chimeric virus are useful for identifying cell lines capable of supporting the replication of these chimeric viruses, in the production of HCV-BVDV virions, for the development of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, in studying the molecular properties of HCV indirectly in vitro, and in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence is encoded by a HCV clone, which is used to construct chimeric concents.
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New nucleic acid comprising a chimeric bovine viral diarrhea virus gen
in which the (non-)structural region has been replaced by hepatitis C
virus (HCV) genome useful for treating or preventing HCV signs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2420 SMSYTWTGALITPCAAEESKLPINPLSNSLLRHHNMYYATTSRSASLRQKKVTFDRLQVL
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                                                                                                          Disclosure; Fig 4G-H; 97pp; English.
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ADO36227 standard; protein; 3010 AA.

ADO3 6227 ID ... σ

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The invention describes a polynucleotide vaccine comprising a polynucleotide sequence (S1) encoding the Hepatitis C virus (HCV) Core polynucleotide sequence (S1) encoding the Hepatitis C virus (HCV) Core protein and at least 1 other HCV protein, and causes expression of the proteins in cells (in which (S1) has been mutated or positioned relative to the polynucleotide sequence encoding the other HCV protein, so that the negative effect of the Core protein on expression of the other HCV protein is reduced). Also described are: a method of preventing the creating an HCV infection in a mammal, comprising administering the cacine cited above to a mammal; and a method of vaccination of an individual, comprising taking a polynucleotide vaccine as cited above, coating the polynucleotide onto gold beads and delivering the gold beads into the skin. HCV nucleic acids, polypeptides, host cells, vectors and antibodies used in the methods, are also disclosed. The polynucleotide vaccine is useful in the manufacture of a medicament for the treatment of HCV. This is the amino acid sequence of the wild type HCV polyprotein.
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                                                                                                                          hepatotropic; virucide; vaccine; gene therapy; vaccine;
Hepatitis C virus; HCV; core protein; HCV infection; vaccination;
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                                                                                         Hepatitis C virus (HCV) J4L6 wild-type polyprotein.
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N-PSDB; ADO36222.
                                                                                                                                                                                                      Hepatitis C virus.
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                                                    26-AUG-2004
                                                                                                                                                                     polyprotein.
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245 QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLFCYLKAA 304
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                   2660 QCCDLAPEARQAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAT
                                                                                    AACRAAKUQDCTMLVNGDDLVVICESAGTQEDAAALRAFTEAMTRYSAPPGDPPQPEYDL
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                                                                  305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                                                                                    ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAMETARHTPVNSWLGNIIMYAPTLM
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N-PSDB; ADO79396.
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Synthetic.
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Sequence 3010 AA

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QCCDLAPEARQAIRSLIERLYIGGPLINSKGONCGYRRCRASGVLITSCGNTLICYLKAT 2719
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Hepatitis C virus; HCV; core protein; HCV infection; vaccination; NS5B.
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                                                                                                                                                     SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
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                                                    SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
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                           Gaps
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 Length 3010;
                           8; Indels
  Score 3015; DB 8;
Pred. No. 1.9e-278;
16; Mismatches 8;
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95.2%;
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 Query Match
Best Local Similarity 95.99
Matches 567; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus
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The invention describes a polynucleotide vaccine comprising a polynucleotide sequence (S1) encoding the Hepatitis C virus (HCV) Core protein and at least 1 other HCV protein, and causes expression of the proteins in cells (in which (S1) has been mutated or positioned relative to the polynucleotide sequence encoding the other HCV protein, so that the megative effect of the Core protein on expression of the other HCV protein is reduced) Also described are: a method of preventing or treating an HCV infection in a mammal, comprising administering the vaccine cited above to a mammal; and a method of vaccination of an individual, comprising taking a polynucleotide vaccine as cited above, coating the polynucleotide onto gold beads and delivering the gold beads into the skin. HCV nucleic acids, polypeptides, host cells, vectors and cantibodies used in the methods, are also disclosed. The polynucleotide vaccine is used in the manufacture of a medicament for the treatment of HCV. This is the amino acid sequence of the HCV NSSB protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
                                                     New Hepatitis C virus (HCV) vaccine having a polynucleotide that encodes the polypeptide sequences of the HCV core and at least one other HCV protein, for use in medicine, particularly for manufacturing a medicament
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 STLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTL
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                                                                                                                                                         Example 2; Page 27; 78pp; English.
                                                                                                                    for treating HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 592 AA;
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GEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLTPI 481 GEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGRYLFNWAVRTKLKLTPI

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PAASQLDLSGWFVAGYSGGDIYHSLSRARPRWFPLCLLLLSVGVGIYLLPNR PAASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR

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304 AAACRAAKLQDCTMLVNGDDLVVICESAGTQBDAASLRVFTEAMTRYSAPPGDPPQPEYD
                                      301 TAACRAAKLODCTWLVNGDDLVVICESAGTQEDAAALRAFTEAMTRYSAPPGDPPQPEYD
                                                                                                         361 LELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIMYAPTL
                                                                                                                                                                         WARMILMTHPFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSP
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                                                                                                                                                       WARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSP
                                                                                                                                                                                                                          GEINRVASCLRKI.GVPPLRVWRHRARSVRAKILSQGGRAAICGKYLFNWAVRTKLKLTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-B hepatitis B virus; NANBV; antigen; infection; diagnosis;
                                                                                                                                                                                                                                                                                                               PAASQLDLSGWFVAGYSGGDIYHSLSRARPRWFPLCLLLLSVGVGIYLLPNR 592
                                                                                                                                                                                                                                                                                           PAASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "envelope protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-A, non-B hepatitis virus polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1863. .2013
/note= "NS4b protein"
2014. .3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "core protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "NS4a protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730. .1006
/note= "NS2 protein"
1007. .1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "NS3 protein"
1616. .1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "NS1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "NS5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                              AAY06423 standard; protein; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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90JP-00230921.
90JP-00305605.
90EP-00314371.
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/note= "en
390. .729
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non-B hepatitis virus.
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31-AUG-1990;
09-NOV-1990;
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27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HCV). The sequence is the translation sequence of a polymucleotide in which codon usage was altered to resemble that of highly expressed human genes. HCV vaccines of the invention comprise a polymucleotide that encodes the HCV proteins Core, NS3, NS4B and NS5B, and does not encode the NS4A and/or NS5A proteins. The proteins may be expressed as individual proteins or as fusion proteins. Preferred fusions include double fusions between NS4B and NS5B and between Core and NS3. The vaccines are useful for the treatment or prevention of an HCV infection.
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                                                                                                                                                                     HCV; NS5B; vaccine; DNA immunisation; hepatotropic; virucide; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is that of the NS5B protein of hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQV
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                                 ADO79389 standard; protein; 592 AA.
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                                                                                                                                    Hepatitis C virus NS5B protein.
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                                                                                                                                                                                                                                                                                                                                                                           15-NOV-2002; 2002GB-00026722.
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569; Conservative
                                                                                                  (first entry)
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                                                                                                                                                                                                                       Hepatitis C virus
Synthetic.
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polypeptide, as predicted from CDMA (see AMX59394) containing the entire open reading frame of the NANBV genome. To obtain this cDNA, NANBV RNAs were extracted directly from NANBV genome. To obtain this cDNA, NANBV RNAs were extracted directly from NANBV genome. To obtain this cDNA, NANBV RNAs broadcaded liver of a patient having NANB hepatitis, or from a resected liver of a patient cancer. The RNA was then converted to double-stranded cDNA, A cDNA library was produced and screened using carum from a patient having chronic name patient having acute NANB hepatitis and serum from a patient having chronic NANB hepatitis. The isolated cDNA allows recombinant production of NANBV antigen polypeptides in microbial or antigens with high purity on a large scale at low cost without the biohazard associated with multiplying virus in animals. Claimed NANBV cucleotide sequences are useful for the recombinant production of polypeptides useful as antigens for vaccines, and as diagnostic reagents. (Updated on 20-MAR-2003 to New hepatitis virus polypeptides, useful for diagnosing and treating hepatitis infections. This sequence represents the non-A, non-B hepatitis virus (NANBV) Claim 2; Fig 2(1)-(16); 56pp; English WPI; 1999-407152/35. N-PSDB; AAX59394.

Sequence 3010 AA;

ö Gaps 0; Length 3010; 95.2%; Score 3014; DB 2; Length 3 96.6%; Pred. No. 2.3e-278; ive 10; Mismatches 10; Indels Query Match
Best Local Similarity 96.69
Matches 571; Conservative

2420 SMSYTWIGALITPCAAEESKIPINALSNSLLRHRNWYYATTSRSAGLRQKKVTFDRLQVL 2479 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124 SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL 65 ઠે g à

δ g ò g ठे 셤 ઠે

AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 3010

AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR

545

2840 ARMILMTHFFSIILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 2899

Search completed: September 22, 2005, 14:47:11 Job time : 172 secs

2480 DDHYRDVLKEMKAKASTVKAKILSVEEACKITPPHSAKSKFGYGAKDVRNLSSKAVNHIH 2539 correct PR field.) 185 2660 g ò 셤 ò 음 ઠે 유 ઠે g

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OM protein - protein search, using sw model

September 22, 2005, 14:40:28 Run on:

8; Search time 19 Seconds (without alignments) 3043.488 Million cell updates/sec

US-10-712-479-2 Title: Perfect score: Sequence:

3167 1 MASMSMSYTWTGALITPCAA.....LLSVGVGIYLLPNRHHHHH

601

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	genome polyprotein										polyr	protein		genome polyprotein	genome polyprotein		genome polyprotein			genome polyprotein	polyprotein - dour	1	٠	1	protein -	protein -	٠	ı	protein -
SUMMARIES	ΩI	GNWVCJ	GNWVTC	A45573	GNWVTW	S18030	S40770	GNWVC3	GNWVCH	JC5620	GNWVJ8	JQ1303	JQ0879	JQ0880	JQ0883	JQ0881	S60587	PS0104	PS0102	D39109	S44214	T08841	T01075	T08839	PC1278	PC1277	PC1274	PC1275	PC1276	PC1279
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عِن	Query Match	95.2	95.2	94.8	93.7	93.0	88.3	87.3	86.0	79.3	75.5	75.1	59.6	55.3	46.5	45.5	30.0	24.4	23.5	22.7	21.1	20.7	20.1	19.9	18.0	17.8	17.7	17.7	17.7	16.2
	Score	3016	3016	3003	2968	2944	2798	2764	2725	2511	2392	2380	1886	1750	1471.5	1442	951	774	744	719	667	654	989	629	569	563	562	562	260	513
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2420 SMSYTWIGALITPCAAEESKLPINPLSNSLLRHHSMVYSTISRSASLRQKKVTFDRLQVL 2479

SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL

Query Match 95.2%; Score 3016; DB 1; Length 3010; Best Local Similarity 96.3%; Pred. No. 3.8e-223; Matches 569; Conservative 12; Mismatches 10; Indels 0

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0; Gaps

64

2480 DDHYRDVLKEMKAKASTVKARLLSIEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 2539

DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR

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NS5 protein - hepa polyprotein - hepa	1 1 1	NSS protein - hepa polyprotein - hepa polyprotein - hepa	hypothetical prote genome polyprotein genome polyprotein	genome polyprotein genome polyprotein	genome polyprotein genome polyprotein genome polyprotein
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30 31	1 E E	35 37	8 6 4 8 6 0	4 4 2 2	4 4 4 5 4 3

ALIGNMENTS

RESULT 1 GNWVCJ GNOGELENS: capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NS5 C; Species: hepatitis C virus C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 C; Accession: A3923; PSOGG6 R; Kato, N; Hijikata, M; Ootsuyama, Y; Nakagawa, M; Ohkoshi, S; Sugimura, T.; Shimotc Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990 A; Reference number: A39253; MUID:91088550; PMID:2175903 A; Reference number: A39253 A; Reference nu	A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence variety. A;Reference number: PS0085 A;Accession: PS0086 A;Accession: AAP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; Scrint C;Acywords: ATP; glycoprotein; hydrolase; nucleotide cPEM> F;116-191/Product: envelope protein B #status predicted cAME> F;192-189/Product: monstructural protein NS1 #status predicted cAMS1> F;191-191/Product: nonstructural protein NS2 #status predicted cAMS2> F;1007-1615/Product: nonstructural protein NS2 #status predicted cAMS2> F;1007-1615/Product: nonstructural protein NS2 #status predicted cAMS2> F;1007-1615/Product: nonstructural protein Mistatus predicted cAMS2> F;1007-1615/Pro	Fi1616-1862/Product: nonstructural protein NS4a #status predicted <n4a> Fi1863-2013/Product: nonstructural protein NS4b #status predicted <n4b> Fi2014-3010/Product: nonstructural protein NS5 #status predicted <ns5> Fi2014-3010/Product: nonstructural protein NS5 #status predicted <ns5> Fi196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,27</ns5></ns5></n4b></n4a>
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C,Accession: A45573
R,Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Hijikata, h Virus Res. 23, 39-53, 199-
A,Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: se A,Reference number: A45573; MUID:92295714; PMID:1318627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A45573
A;Status: preliminary
A;Modecule type: DNA
A;Residues: 1-3010 cTAN>
A;Cross-references: UNIPKOT:000269; GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1; I
A;Experimental source: HCV-JT
A;Experimental source: HCV-JT
A;Note: sequence extracted from NCBI backbone (NCBIN:106206, NCBIP:106207)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine
C;Keywords: ATP; glycoprotein; M#status predicted <ERPN>
F;10-119/Product: capsid protein M #status predicted <MEE>
F;2-115/Product: major envelope protein NSI #status predicted <NSI>
F;30-129/Product: nonstructural protein NSI #status predicted <NSI>
F;30-1006/Product: nonstructural protein NSI #status predicted <NSI>
F;30-123/Product: nonstructural protein NSI #status predicted <NSI>
F;110-1317/Region: nucleotide-binding motif B
F;1312-1317/Region: nucleotide-binding motif B
F;1312-1317/Region: nucleotide-binding motif B
F;1312-1317/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                            2600 TLPQVVMGSSYGFQXSPGQRVEFLVNTWKSKRNPMGFSYDTRCFDSTVTENDIRVEESIX 2659
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                              2480 DDHYRDVLKEMKAKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIH 2539
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                          QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA
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N;Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructure)

N;Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructure)

C;Species: hepatitis C virus

C;Species: hepatitis C virus

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: A38465

R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, B.;
J. Virol. 65, 1105-1113, 1991

A;Reference mumber: A38465; MUID:91140698; PMID:1847440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: genomic RNA
A; Residues: 1-3010 «TAK»
A; Residues: 1-3010 «TAK»
A; Residues: 1-3010 «TAK»
A; Cross-references: UNIPROT:P26663; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g3297
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F; 2-115; Product: capsid protein C #status predicted «CEP»
F; 116-191; Product: major envelope protein M #status predicted «MEE»
F; 130-195; Product: major envelope protein RS1 #status predicted «MSI»
F; 130-1006; Product: nonstructural protein NS2 #status predicted «NS2»
F; 120-1137; Region: nucleotide-binding motif A (P-loop)
F; 1310-1319; Region: DEXH motif
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,22
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                         2540 SVWEDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2599
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genome polyprotein - hepatitis C virus (isolate JK1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (BC 3.4.21.98) (nonstructur)
Dyocein NS44; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
A;Variety: isolate JK1
C;Date: 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #text_change 09-Jul-2004
C;Accession: S18030; S33570; A48332; S18029
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: A whole genome of hepatitis C virus CDNA was isolated from a single patier A;Reference number: S18028
A;Accession: S18030
A;Molecule type: genomic RNA
A;Residues: 1-3010 <ARNA
A;Residues: 1-3010 <ARNA
A;Residues: 1-3010 <ARNA
A;Cross-references: UNIPROT:068949; EMBL:X61596; NID:g59478; PIDN:CAA43793.1; PID:g59479
A;Ridda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
A;Ch. Virol. 128, 163-169, 1993
A;Reference number: A4832; MUID:93119270; PMID:8380322
A;Accession: S33570
A;Accession: Sa3570
A;Accession: S33570
A;Accession: S33570
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A;Accession: S33570
A;Accession: Sayonacces in Sayonacces i
   F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,233,234,250;305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
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                                                                                                                                   Length 3010;
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                                                                                                                                Query Match 93.7%; Score 2968; DB 1;
Best Local Similarity 94.9%; Pred. No. 1.9e-219;
Matches 561; Conservative 15; Mismatches 15;
                                                                                                                             93.7%; Score 2968;
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A; Residues: 1-3010 < CHE>
A; Cross = references: UNIPROT: P29846; GB: M84754
A; Cross = references: UNIPROT: P29846; GB: M84754
A; Cross = references: UNIPROT: P29846; GB: M84754
C; Superfamily: hepatitis C virus genome polyprotein
C; Reywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F; 116-191/Product: capsid protein C #status predicted < REPN
F; 192-389/Product: molor envelope protein B #status predicted < NES>
F; 390-7729/Product: nonstructural protein NS1 #status predicted < NS1>
F; 730-1006/Product: nonstructural protein NS2 #status predicted < NS2>
F; 730-1207/Region: nucleotide-binding motif A (P-loop)
F; 1312-1317/Region: nucleotide-binding motif B
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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A;Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92230206; PMID:1314449
A;Accession: A40244
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C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                2420 SMSYTWTGALITPCAAEESKLPINALSNSLLRHINNVYATTSRSASLROKKVTFDRLOVL
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                                                                                            SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLRQKKVIFDRLQVL
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                                9; Indels
95.9%; Pred. No. 3.8e-222; tive 15; Mismatches 9;
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                                567; Conservative
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   Local Similarity
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A;Cross-references: GB:D00831; NID:g221511; PIDN:BAA00705.1; PID:g221512
A;Experimental source: isolate HC-J1
C;Superfamily: heaptitis C virus genome polyprotein
C;Superfamily: heaptitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein B #status predicted <MED>
F;130-139/Product: major envelope protein E #status predicted <MED>
F;390-729/Product: nonstructural protein NSI #status predicted <NSI>F;730-1006/Product: nonstructural protein NSI #status predicted <NSI>F;130-1237/Region: nucleotide-binding motif B (P-loop)
F;1312-131//Region: nucleotide-binding motif B
                                                                                                                                                            A; Molecule type: genomic RNA
A; Residues: 1-3011 < OKA>
A; Cross-references: UNIPROT: 003463; EMBL: D10749; NID: g221586; PIDN: BAA01582.1; PID: g22158
B; Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990
A; Title: The S'-terminal sequence of the hepatitis C virus genome.
A; Reference number: PC1284; MUID: 91013116; PMID: 2170712
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S40770; PC1285
R;Okamoto, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2601 KLPPAVMGSSYGFQYSPGQRVEFLVQAWKSKRTPMGFSYDTRCFDSTVTESDIRTEEAIY
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88.8%; Pred. No. 2.3e-206;
cive 28; Mismatches 38;
                                                                               submitted to the EMBL Data Library, March 1992
A;Reference number: S40770
A;Accession: S40770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1316-1319/Region: DEXH motif
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                                             A.Note: this sequence is inconsistent with the nucleotide translation
A.Note: this sequence is inconsistent with the nucleotide translation
A.Note: the authors translated the coden AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TrC for residue 711 as Ser
A.Note: sequence extracted from NGBI backbone (NCBIN:121747, NCBIP:121748)
C.Superfamily: hepatitis C virus genome polyprotein
C.Superfamily: hepatitis C virus genome polyprotein
C.Seywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; F:2-115/Product: capsid protein C #status predicted <CPC>
F:10-191/Product: envelope protein E #status predicted <NES>
F:10-191/Product: major envelope protein E #status predicted <NSS>
F:1007-161/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-161/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-161/Product: nucleotide-binding motif B
F:1310-1237/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;186,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (As
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
Ç;Species: hepatitis C virus
  A;Residues: 1-547,'T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOW>
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                            A; Cross-references: EMBL:X61591
                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1316-1319/Region: DEXH motif
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559; Conservative
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genome polyprotein - hepatitis C virus (strain H)
N,Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructum
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
;196,209;234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,236
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A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A36814; A41546
E;Inchauspe, G; Zebedee, S; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992
A;Description: GenBank, July 1992
A;Reference number: A36814
                                                                                                 2421 SMSYSWTGALVTPCAAEEQKLPINALSNSLLRHHNLVYSTTSRSACQRKKKVTFDRLQVL 2480
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      2661 QCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCGYRRCRASGVLTTSCGNTLTCYIKAR 2720
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                                                                                                                                                                                                                                                                                                                              425 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG
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                                                                                                                                                                                              ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                      305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: genomic RNA
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
F;116-191/Product: canyelope protein M #status predicted cRNS>
F;192-398/Product: major envelope protein RS1 #status predicted cNS2>
F;1007-161s/Product: nonstructural protein NS2 #status predicted cNS2>
F;1007-161s/Product: hepacivirin #status predicted cNS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1316-1317/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: A39166
A,Accession: A39166
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Reaidues: 1-3011 cCHO>
A,Cross-references: UNIPROT:P26664; GB:M62321; NID:g329873; PIDN:AAA45676.1; PID:g329874
A,Cross-references: UNIPROT:P26664; GB:M62321; NID:g329873; PIDN:AAA45676.1; PID:g329874
A,Cross-references: UNIPROT:P26664; GB:Mc B.; Peutherer, J.F.; Follett, E.; Yap, P.I.
A,Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e
A,Reference number: PQ0393; MUID:92268871; PMID:1316939
A,Accession: PQ099
A,Mc B,Cross-references: DDBJ:D10128
A,Residues: 1577-1633 cCHA>
A,Residues: 1577-1633 cCHA>
A,Residues: 1577-1633 cCHA>
A,Residues: 1577-1633 cCHA>
A,Residues: 1577-1630 cCHA>
A,Residues: 1577-1630 cCHA>
A,Recession: PQ0404
                                                                                                                                                                                                               genome polyprotein - hepatitis C virus (strain HCV-1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS4s, nonstructural protein NS4s, nonstructural protein NS5s
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Accession: A39166; P00403; P00404
R;Choo, Qil.; Richman, K.H.; Han, J.H.; Berger, K; Lee, C.; Dong, C.; Gallegos, C.; Coi Proc. Natl. Acad. Sci. U.S. A. 88, 2451-2455, 1991
A;Title: Genetic organization and diversity of the hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
151863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NSS>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NSS>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2077,22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2541 SVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVT 2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TLPQAVMGSSYGPQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVERSIY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
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                                 2961 AAGRLDLSGWFTAGYSGGDIYHSVSHARPRWFWFCLLLLAAGVGIYLLPNR 3011
545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.3%; Score 2764; DB 1; Length 3011; Best Local Similarity 87.5%; Pred. No. 9.6e-204; Matches 517; Conservative 32; Mismatches 42; Indels 0
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2904 EINRVASCLRKLGVPPLRAWRHRARAVRAKLIAQGGRAAICGIYLFNWAVKTKRKLTPLA 2963
             425 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                                                                                                                                                         245 QCCDLAPEARQAIRSLIERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLICYLKAA
                                                                                                                                                                                                                                             2664 QSCDLQPEARVAIRSLTQRLYCGGPMYNSKGQQCGYRRCRASGVFTTSMGNTWTCYIKAL
                                                                                                                                                                                                                                                                                                     305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                                                                                                                       185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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N;Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructury brotein N34a; nonstructural protein N34b; nonstructural protein N35s
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
R;Chamberlain; R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A;Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant A;Reference number: JC5620; MUID:97366593; PMID:9223423
                                                                                                                                                                                                                                                                                                 2541 SV#KDLLEDSVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2600
                                                                                   QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                                                                                                                                                           ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
                                                                                                                                                                                                                                                                                                                                                         EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP 544
           SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                    2901 EINRVAACLRKLGVPPLRAWRHRAWSVRARILARGGKAAICGKYLFNWAVRTKLKLTPIT
                                                                   185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                    AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
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ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLM

EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP

2783

304

184

SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS

DDHYRDVLKEMKAKASTVKAKLLSVBEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR

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Genome polyprotein - hepatitis C virus (strain HC-J8)

N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructur)

N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructur)

protein N842; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40250; PQ0397; PQ0859
R;Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamoto, K.; Lizuka, H.; Tanaka, T.; Fukuda, S.; Virology 188, 331-341, 1992
A;Ricle: Pull-length sequence of a hepatitis C virus genome having poor homology to repoin A;Reference number: A40250; MUID:92230232; PMID:1314459
A;Residues: 1-3033 < OKAA,
A;Residues: 1-3033 < OKAA,
A;Residues: 1-3033 < OKAA,
A;Cross-references: UNIPROT:P26661; GB:D10988; GB:D01221; NID:g221608; PIDN:BAA01761.1; F R;Chan, S. W.; McChain, F. 
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A; Residues: 2678-2754 CHA>
A; Residues: 2678-2754 CHA>
A; Cross-references: DDBJ 1010134
A; Experimental source: isolate E-b12
R; Kato, N: Ootsuyama, Y:; Ohkoshi, S:; Nakazawa, T:; Mori, S:; Hijikata, M.; Shimotohno, Biochem: Biophys: Res. Commun. 181, 279-285, 1991
A; Title: Distribution of plural HCV types in Japan.
A; Reference number: PQ0554; MUID: 92068204; PMID: 1720309
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A;Molecule type: mRNA
A;Residues: 2678-2729 <KAT>
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A; Residues: 1-3014 <CHA>
A; Residues: 1-3014 <CHA>
A; Chastales: 1-3014 <CHA
A; Residues: 1-3014 <CHA
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Best Local Similarity 78.8 Matches 466; Conservative

Query Match

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A;Reference number: JQ1303; MUID:92044440; PMID:1658196
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A;Cross-references: GB:D10562; GB:D90518; NID:g221523; PIDN:BAA01418.1; PID:g221524
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: AFP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F;116-191/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <NBS>
F;123-289/Product: major envelope protein B #status predicted <NBS>
F;34-101/Product: nonstructural protein NS1 #status predicted <NS2>
F;131-151/Product: nonstructural protein NS2 #status predicted <NS2>
F;131-151/Froduct: hepacivirin #status predicted <NS3>
F;131-131/Region: nucleotide-binding motif A (P-loop)
F;1320-1323/Region: nucleotide-binding motif B F;1320-1323/Region: nucleotide-binding motif B F;1320-1323/Region: nucleotide-binding motif B F;1320-1323/Region: nucleotide-binding motif B F;1320-1333/Region: nonstructural protein NS48 #status predicted <NAS>
F;1867-2017/Product: nonstructural protein NS48 #status predicted <NSS>
F;196,209,233,239,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVWKDILEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
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                                                                                                                                                                                                                                                                                                 / Match 75.5%; Score 2392; DB 1; Length 3033; Local Similarity 75.5%; Pred. No. 4.2e-175;
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                                                                                                                                                                                                                                                                                                                                   59; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                   Matches 446; Conservative
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A; Molecule type: genomic RNA
A; Residues: 1-3033 < CKA>
A; Residues: 1-3045 < CKA>
A; Residues: 1-3045 < CKA>
A; Experimental source: isolate HC-36 from a Japanese individual
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: nargid protein C #status predicted < CRC>
F; 115-191/Product: envelope protein M #status predicted < NSI>
F; 330-733/Product: nonstructural protein NSI #status predicted < NSI>
F; 1316-1321/Region: nucleotide-binding motif B
F; 1316-1321/Region: nucleotide-binding motif B
F; 1320-1323/Region: DEXH motif
F; 1650-1866/Product: nonstructural protein NS4 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS4 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS4 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS4 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS4 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
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F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nonstructural protein NS5 #status predicted < NAB>
F; 1867-2017/Product: nons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2683 RACSLPEEAHTAIHSLTERLYVGGPMFNSKGQTCGYRRCRASGVLTTSMGNTITCYVKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TLPQAVMGSSYGFOXSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2623 KLPQAVMGASYGFQYSPAQRVBFLLKAWAEKKDPMGFSYDTRCFDSTVTERDIRTEESIY
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NSS protein - hepatitis C virus (strain J4) (fragment)
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 12-Peb-1993 #sequence_revision 12-Peb-1993 #text_change 09-Jul-2004
C;Accession: JQ0879
R;Okamoto, H.

RESULT 12

JQ0879

genome polyprotein - hepatitis C virus (isolate HC-J6)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JQ1303
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.; Machida, A.; Miyakawa, Y.
J. Gen. Virol. 72, 2697-2704, 1991
A;Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a hum

JQ1303

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3'-terminal sequences of the genomic RNA of hepatitis
                                                                                                                                                       HGLSAFSLHSYSPGEINRVAACLRKLGVPPLRAWRHRARSVRARLLSRGGRAAICGKYLF 300
                                                                                                                                                                                                         NWAVRTKLKLTPIPAASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIY 590
                                                                                                                                                                                                                            195 YGFQYSPKQRVEFLVNTWKAKKCPMGF-SYDTRCFD-STVTENDIRVEESIYQCCDLAPE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
 HGLSAFSLHSYSPGEINRVASCLRXLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLF 530
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                                                                                                                                                                                                                                                                                                                                                                                                         Genome polyprotein - hepatitis C virus (strain J7) (fragments)
N;Contains: NS5 protein
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0883
R;Okamoto, H.
R;Okamoto, H.
A;Description: The S'-terminal and 3'-terminal sequences of the genomic RNA
A;Reference number: JQ0879
                                                                            487 YCWHYPPK------PCGIVSAKTVCGPVYTVTERDIRTEESIYQACSLPQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 QDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDLELITSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 NVSVAHDASGKRVYYLIRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLWARMILMTH
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Best Local Similarity 70.0%; Pred. No. 5.6e-105;
Matches 282; Conservative 40; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: JQ0883
A,Molecule type: genomic RNA
A,Residues: 1-874 <OKA>
A,Cross-terences: UNIPROT:Q7LZX6
A,Experimental source: strain J7
C,Superfamily: hepatitis C virus genome polyprotein
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NSS proctain - hepatitis C virus (strain J1) (fragment)

C)Species: hepatitis C virus

C)Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C)Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C)Date: 12-Feb-1993

R)Accession: JQ0880

A)Reference number: JQ0879

A)Accession: JQ0880
                       hepatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLF 530
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                     genomic RNA
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                                                                                                                                                                                                                                                             231 TVTENDIRVEESIYQCCDLAPEARQAIRSLIERLYVGGPMTNSKGQNCGYRRCRASGVLT
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                     of the
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88.2%; Pred. No. 6.1e-127;
tive 23; Mismatches 20; Indels
           A; Description: The S; terminal and 3'-terminal sequences of A; Reference number: JQ0879
A; Rocession: JQ0879
A; Molecule type: genomic RNA
A; Residues: 1-365 < OKA>
A; Cross-references: UNIPROT: Q81717
A; Experimental source: strain J4
C; Superfamily: hepatitis C virus genome polyprotein
                                                                                                                                                                                    Score 1886; DB 2;
Pred. No. 2.1e-137;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Residues: 1-365 < OKA>
A,Ross-references: UNIPROT:Q81716
A,Experimental source: strain J1
C,Superfamily: hepatitis C virus genome polyprotein
                                                                                                                                                                                    Query Match
Best Local Similarity 96.7%;
Matches 353; Conservative
submitted to JIPID, January 1991
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Matches
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셤 ò 요 &

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Occupance polyprotein - hepatitis C virus (strain J6) (fragments)
NiContains: NSS protein
NiContains: NSS protein
Cispecies: hepatitis C virus
Cispecies: hepatitis
Cispeciption: The S'-terminal and 3'-terminal sequences of the genomic RNA A; Reference number: JQ0879
A; Reference number: JQ0879
A; Reference number: JQ0879
A; Recession: J0874 < CoKA-
A; Residues: l-874 < CoKA-
A; Coss = references: UNIPROT:Q7LZYS
A; Reperimental source: strain J6
C; Superimental source: strain J6
C; Superimental source: strain J6
C; Superimental source: strain J6
C; Reywords: polyprotein
C; Reywords: polyprotein
F; 510-874/Product: NS5 protein (fragment) #status predicted <NS5>
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Q99au2 hepatitis c Q9j3f9 hepatitis c Q02028 hepatitis c Q9dtd9 hepatitis c Q9j3h7 hepatitis c Q90mb6 hepatitis c Q90mb6 hepatitis c Q80mb5 hepatitis c Q90mb5 hepatitis c Q90y3 hepatitis c Q9qy3 hepatitis c

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"Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited."; Hepatol. Res. 20:161-171 (2011).

EMBL; AB049091; BAB18804.1; -...

PIR; AR0196; A61196.

PIR; PS0329; PS0329.

HSSP; Q81755; 1DXP.
                                                                                                                                                                                                                                                                                                                                                                                                                               Hepātitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Sertum;
Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R GO; GO: 0016021, C: integral to membrane; IEA.
R GO; GO: 0019028; C: viral capsid; IEA.
R GO; GO: 0019021; C: viral capsid; IEA.
GO; GO: 0019031; C: viral capsid; IEA.
GO; GO: 0005032; F: RATP-dependent helicase activity; IEA.
GO; GO: 00016787; F: RATP-dependent helicase activity; IEA.
GO; GO: 00016787; F: RATP-dependent helicase activity; IEA.
GO; GO: 0001878; F: RNA-directed RNA polymerase activity; IEA.
GO; GO: 0001896; F: RNA-directed RNA polymerase activity; IEA.
GO; GO: 0001896; F: RICHOLUTEAL molecule activity; IEA.
GO; GO: 0001896; F: RICHOLUTEAL molecule activity; IEA.
GO; GO: 0001897; P: protecolysis and peptidolysis; IEA.
GO; GO: 0018079; P: viral genome replication; IEA.
R GO; GO: 0019087; P: viral transformation; IEA.
R INTERPRO; IPRO01410; DEAD.
ENTREPRO; IPRO01410; DEAD.
ENTREPRO; IPRO01410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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POLG HCVJT
Q9QI<u>Y</u>3
Q9QIY4
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HCV_RdRP.
Helfcase.C.
Peptidase_S29.
Peptidase_Cys.
Pept_U39_HCV_NS2.
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Q99AU2
Q9J3F9
Q02828
                                            Q9DTD9
Q9J3H7
P90193
P90193
Q80MH6
Q9WMX2
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HCV_capsid.
HCV_core.
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InterPro; IPR002521;
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InterPro; IPR002518;
 Polyprotein.
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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081817
POLG HCVBK
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Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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1: uniprot_sprot:*
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n; PF022907; HCV_NS3; 1.

n; PF01006; HCV_NS4s; 1.

n; PF01001; HCV_NS5s; 1.

pF01506; HCV_NS5s; 1.

n; PF00271; Helicase C; 1.

n; PF00998; Viral_RdRP; 1.
                                                                                                                                                                                                                                                             QBJYS1; 1CWX
                                                                                                    SEQUENCE FROM N.A.
                                                         NCBI_TaxID=11103;
    Hepatitis C virus
                                                                                                                     STRAIN=MD12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
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    2420 SMSYTWTGALITPCAAEESKLPINALSNSLIRHHNWYYATTSRSASLROKKVTFDRLQVL 2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2600 TLPQAVMGSSYGRQYSPQQRVEFLVKTWKSKKCPMGFSYDTRCFDSTVTENDIRVEESIY 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2660 QCCDLAPEARQAIRSLTERLYIGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAT 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2720 AACRAAKIQDCIMIVNGDDLVVICESAGTQEDAANIRVFTEAMTRYSAPPGDPPQPEYDL 2779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITSCSSNVSVAHDASGKRVYYLIRDPTTPLSRAAMETARHTPVNSWLGNIMYAPTLM 2839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 ARMILMTHFFSILLLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLPNWAVRTKLKLTPIP 544
                                                                       | Pfam; PF0139; HCV = COLF; | Pfam; PF0139; HCV = COLF; | Pfam; PF01399; HCV = COLF; | Pfam; PF01399; HCV = COLF; | Pfam; PF01399; HCV = COLF; | Pfam; PF01390; HCV = COLF; | Pfam; PF01390; HCV = COLF; | Pfam; PF01000; HCV = COLF; | Pfam; PF01000; HCV = COLF; | Pfam; PF00399; Vixal RdRp; | Pfam; PF00399; Vixal RdRp; | Pfam; PF00399; Vixal RdRp; | Pfam; PF00399; Pfam; PF00399; Pfam; PF00399; Pfam; Pf00399; Pfam; Pf00399; Pf0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2480 DDHYRDVLKEMKAKAKSTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRNLSSKAINHIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLRQKKVIFDRLQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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                                                                                                                                                                                                                                                                                                                                                                                                96.0%; Score 3040; DB 2; Length 3010; 97.1%; Pred. No. 6.3e-228; tive 11; Mismatches 6; Indels 0
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PS_ir.
Pam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 97.1%
Matches 574; Conservative
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09J310 PRELIMINARY; PRT; 3010 AA. 09J310; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Polyprotein.

22444

RESULT 2 Q9J3I0

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2420 SMSYTWTGALITPCAAEESKIPINALSNSLIRHINWYYATTSRSACQRQKKYTFDRLQVL 2479
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                                                                                                                                                                                                                  Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF207753; AAF65943.1; -.
PIR; P00246; A61196.
PIR; P00246; P00246.
PIR; PS0329; PS0329.
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PROSTIE; BS00190; CTYOCHROME C; UNKNOWN_1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO: 0016021; C:uintegral to membrane; IEA.
R GO; GO: 0016021; C:uintegral to membrane; IEA.
R GO; GO: 0019028; C:viral capsid; IEA.
R GO; GO: 0019028; C:viral capsid; IEA.
R GO; GO: 00005124; F:ATP-binding; IEA.
R GO; GO: 00007125; F:ATP-dependent helicase activity; IEA.
R GO; GO: 00007125; F:RATP-dependent helicase activity; IEA.
R GO; GO: 00005126; F:RATP-dependent helicase activity; IEA.
R GO; GO: 00005126; F:Serine-type peptidase activity; IEA.
R GO; GO: 00005126; F:Serine-type peptidase activity; IEA.
R GO; GO: 00005126; F:Serine-type peptidase activity; IEA.
R GO; GO: 00105019; P:uiral genome replication; IEA.
R GO; GO: 0019079; P:uiral genome replication; IEA.
R GO; GO: 0019079; P:viral genome replication; IEA.
R InterPro; IPR001410; DEAD.
R InterPro; IPR001521; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002511; HCV_NSA.
R InterPro; IPR001490; HCV_NSA.
R InterPro; IPR001490; HCV_NSA.
R InterPro; IPR001490; HCV_NSA.
R InterPro; IPR001516; HCV_NSA.
R InterPro; IPR001516; HCV_NSA.
R InterPro; IPR001516; HCV_NSA.
R InterPro; IPR001516; HCV_NSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IFROUGLES; HCV RORF.
Interpro; IPRO01650; Helfcase C.
Interpro; IPRO04109; Peptidase S29.
Interpro; IPRO04003; Pept Ser Cys.
Interpro; IPRO07095; RNA_DOL_DS_PS.
Interpro; IPRO07095; RNA_DOL_DS_PS.
Interpro; IPRO07094; RNA_DOL_PSVIT.
Pfam; PFO1542; HCV_capsid; 1.
Pfam; PFO1542; HCV_capsid; 1.
Pfam; PFO1559; HCV_capsid; 1.
Pfam; PFO1559; HCV_env; 1.
Pfam; PFO1559; HCV_NSI; 1.
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BINRVASCLRKIGVPPLRVWRHPARSVRAKILSQGGRAAICGKYLFNWAVRTKLKITPIP 544
                                                            Interproj irruvizzazi HCV cap81d.

BR Interproj IPR002521; HCV_core.

BR Interproj IPR002531; HCV_core.

BR Interproj IPR002531; HCV_NS1.

BR Interproj IPR00145; HCV_NS4.

BR Interproj IPR00146; HCV_NS4.

BR Interproj IPR001409; Peptidase S29.

BR Interproj IPR0010409; Peptidase S29.

BR Interproj IPR0010409; Peptidase S29.

BR Interproj IPR0010409; Peptidase S29.

BR Interproj IPR001093; Peptidase S29.

BR Interproj IPR001093; Peptidase S29.

BR Interproj IPR001094; RNA_pol_PSVIr.

BR Edm; PP01543; HCV_core; 1.

BR Edm; PP01543; HCV_core; 1.

BR Edm; PP01549; HCV_NS2; 1.

BR Edm; PP01569; HCV_NS2; 1.

BR Edm; PP01001; HCV_NS3; 1.

BR Edm; PP01001; HCV_NS4; 1.

BR Edm; PP01001; HCV_NS4; 1.

BR Edm; PP01001; HCV_NS4; 1.

BR Edm; PP00271; Helicase C; 1.

BR Edm; PP00298; Viral RGRP; 1.

BR MRAT; SM00487; BEXDE; 1.

BR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

ROCAT POTOLEIN; Envelope Protein; Glycoprotein; Nonstructural protein; S0 SBOUENCE S101 AAP. 37775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 DDHYRDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.0%; Score 3039; DB 2; Length 301 Best Local Similarity 97.6%; Pred. No. 7.5e-228; Matches 577; Conservative 7; Mismatches 7; Indels
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                            DEAD/DEAH N
HCV_capsid.
HCV_core.
                                  InterPro; InterP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365
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                                                                                                                                         2600 TLPQAVMGSSYGFQYSPGQRVEFLVNTWKSKKCPMGFSYDTRCFDSTVTENDIRVEESIY 2659
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SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
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MEDLINE-98122498; PubMed=9462666; DOI=10.1002/hep.510270242;

MALSAIR H., AOKI Y., Harada T., Ishil K., Suzuki T., Nagamori S.,

Toda G., Matesuura Y., Miyamura T.;

Toda G., Matesuura Y., Miyamura T.;

"Pull-length complementary DNA of hepatitis C virus genome from an infectious blood sample.";

Hepatology 27:621-627(1998).

EMBL; D89815; BAA25076.1; -.

REMEL; D89815, A61196.

RIK; PQ0804; PQ0804.

RIK; PQ0804; PROBER C. INTEGRAL OF MEMbrane C. IEA.

RO; GO:0019031; C:viral capsid; IEA.

RO; GO:0003703; F:RNA binding; IEA.

RO; GO:0003703; F:RNA-directed RNA polymerase activity; IEA.

RO; GO:0003703
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
   2960 EASQLDLSGWFVAGYSGGDIYHSLRARPRWFWWCLLLLSVGVGIYLLPNR 3010
545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 595
                                                                       Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
                            Q9DTE9,
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein.
                         PRT; 3010 AA
                         PRELIMINARY;
                                                                SEQUENCE FROM N.A.
                                                                    TISSUE=Serum;
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2420 SMSYTWTGALITPCAAEESKIPINALSNSLLRHHNMIYATTSRSAGLRQKKVTFDRLQVL 2479
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MEDLINE=93359897; PubMed=8394876;
MEDLINE=93359897; PubMed=8394876;
Mang Y., Okamoto H., Tsuda F., Nagayama R., Tao Q.M., Mishiro S.;
"Prevalence, genotypes, and an isolate (HC-C2) of hepatitis C virus in Chinese patients with liver disease.";
J. Med. Virol. 40:254-260(1993).
BEMBL; D10934; BAA01728.1; -.
PIR; A61196; A61196.
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SWART; SM00487; DEXDC; 1.

PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Pelyprotein; Transmembrane.

SEQUENCE 3010 AA; 326780 MW; 668CFFEASFEC3658 CRC64:
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Hepacivirus.
NCBI_TaxID=11103;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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2780 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIMYAPTLW 2839
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             2660 QCCDLAPEAKQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS 2719
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MEDLINE-20391112; PubMed=1325713;
MEDLINE-20391112; PubMed=1325713;
MEDLINE-20391112; PubMed=1325713;
McDucto H., Kojima M., Okada S., Yoshizawa H., Iizuka H., Tanaka T.,
Muchmore E.E., Peterson D.A., Ito Y., Mishiro S.;
"Genetic drift of hepatitis C virus during an 8.2-year infection in a chimpanzee: variability and stability.";
Chimpanzee: variability and stability.";
EMBL; D13558; BAA02756.1; -.
PIR; R61196, A61196.
PIR; PQ0246; PQ0246.
PIR; PS0329; PS0329.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0000326; F:ATP-dependent helicase activity; IEA.

GO; GO:0000326; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0000396; P:Princutural molecule activity; IEA.

R GO; GO:000530; P:princutural molecule activity; IEA.

R GO; GO:000530; P:ranscription; IEA.

R GO; GO:0019087; P:viral genome replication; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
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InterPro; IPR001410; DEAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
R PIR; P00254; P00254.

R PIR; P00804; P08064.

R PIR; P00804; P00804.

R GO; GO:0019021; C:integral to membrane; IEA.

GO; GO:0019021; C:viral capaid; IEA.

GO; GO:0019021; C:viral capaid; IEA.

GO; GO:0019021; C:viral capaid; IEA.

GO; GO:000326; F:ATP binding; IEA.

GO; GO:000326; F:ATP binding; IEA.

GO; GO:000326; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:001908; F:RNA-directed RNA polysis; IEA.

GO; GO:0019087; P:Viral genome replication; IEA.

R InterPro; IPR001410; DEAD.

R InterPro; IPR001522; HCV_capsid.

R InterPro; IPR001521; HCV_capsid.

R InterPro; IPR001521; HCV_Capsid.

R InterPro; IPR00156; HellCase_C.

R InterPro; IPR00150; HellCase_C.

R InterPro; IPR001650; HellCase_C.

R InterPro; IPR001650; HellCase_C.

R InterPro; IPR001650; RNA-pol_BS-PE.

R InterPro; IPR001991; RNA-pol_BS-PE.

R InterPro; IPR001991; RNA-pol_BS-PE.

R InterPro; IPR001991; RNA-pol_BS-PE.

R Pfam; PF01543; HCV_capsid; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, Transmembrane.
3010 AA; 326857 MW; EA7D306A4BA2E224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01539; HCV-env; 1.
Pfam; PF01560; HCV-NS1; 1.
Pfam; PF01581; HCV-NS2; 1.
Pfam; PF02907; HCV-NS3; 1.
Pfam; PF01006; HCV-NS48; 1.
Pfam; PF01001; HCV-NS48; 1.
Pfam; PF01001; HCV-NS48; 1.
Pfam; PF00271; Helfcase_C; 1.
Pfam; PF00998; Viral RARP; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyprotein;
SEOUENCE 3
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SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLROKKVTFDRLQVL
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                                                                                268285;
                                                      068285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2480 DDHYRDVLKEMKAKASTVKAKLLSIEEACKLTPPHSAKSKFGYGAKDVRNLSSRAVNHIR 2539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2540 SVWEDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2600 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKSKKCPMGFSYDTRCFDSTVTESDIRVEESIX 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2780 ELITSCSSNVSVAHDASGKRVYYLTRDPTIPLARAAWETARHTPVNSWLGNIMYAPALW 2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDHYRDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPQAVMGSSYGPQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
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InterPro; IPR004109; Peptidase S29.

R InterPro; IPR009003; Pept_Ser_Cys.

R InterPro; IPR00709518; Pept_U39 HCV NS2.

R InterPro; IPR007094; RNA_DOI_DS_PS.

R InterPro; IPR007094; RNA_DOI_PSVir.

R Pfam; PP01543; HCV_core; 1.

R Pfam; PP01539; HCV_core; 1.

R Pfam; PP01539; HCV_NS1; 1.

R Pfam; PP01539; HCV_NS2; 1.

R Pfam; PP01006; HCV_NS3; 1.

R Pfam; PP01009; Urial RRP; 1.

R Pfam; PP01099; Urial RRP; 1.

R Pfam; PP01099; Urial RRP; 1.

R PROSITE; PS00190; CTYCOHROME C; UNKNOWN 1.

R POLYCEIN; ENVelope protein; Glycoprotein; Nonstructural protein; MP POLYCEIN; TANDERNERS.

T CHAIN 1007 1615 NS3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.7%; Score 3030; DB 2; Length 3010; Best Local Similarity 96.4%; Pred. No. 3.8e-227; Matches 570; Conservative 16; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 E protein.
29 NS1/E2 protein.
326959 MW; 93D465526F3EADF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                NS2 protein.
NS3 protein.
C protein.
NS4 protein.
NS5 protein.
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3010 AA;
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SEQUENCE
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Coat protein; Bruvelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SEQUENCE 3010 AA; 326915 MW; 29B306FCSBBEBC9E CRC64;
                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MNR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepativirus.
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                                                                                                                                                                                     Cho J., Park Y., Lee Y., Yang J., Ryu W.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U16362; AAA52748.1; -.
PIR; AG1196; AG1196.
PIR; PS0329; PS0329.
HSSP; Q81755; IDXP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3010 AA; 326915 MW; 29B306FC5B8EBC9E CRC64;
PRT; 3010 AA
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Pfam: PF01560; HCV env; 1.
Pfam: PF01560; HCV NS1; 1.
Pfam: PF01507; HCV NS2; 1.
Pfam: PF01006; HCV NS4; 1.
Pfam: PF01006; HCV NS4s; 1.
Pfam: PF01506; HCV NS4s; 1.
Pfam: PF01506; HCV NS5s; 1.
Pfam: PF00571; Helicase C; 1.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00487; DEXDC;
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InterPro;
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                                                                    DDHYRDVLAEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVTHIR 2539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLW 2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2900 EINRVASCLRKLGVPPIRAMRHRARSVRAKLLSQGGRAATCGKYLFNWAVRTKLKLTPIP 2959
2420 SMSYTWTGALITPCAAEESKLPINPLSNSLLRHHNWYYATTSRSAGLRQKKVTFDRLQVL 2479
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                                                                                                                                         SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                               AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
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                                              DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
MRNA, complete cds.
Hepatitis C virus.
Hepatitis C virus.
Hepatitis PaskNA positive-strand viruses, no DNA stage; Flaviviridae;
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Cho J.-M.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.

R BEBL; M95362; AAA45721.1; -.

R PIR; A61196; A61196.

R PIR; A61196; A61196.

R PIR; PS0329; PS0329.

R HSSP; Q81755; 1DXP.

GO; GO:0010021; C:intrgral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0003524; F:ATP binding; IEA.

GO; GO:0003524; F:ATP binding; IEA.

GO; GO:0003526; F:RNA-dependent helicase activity; IEA.

GO; GO:0003526; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003526; F:serine-type peptidase activity; IEA.

GO; GO:0005508; P:proteolysis and peptidolysis; IEA.

GO; GO:0005508; P:transcription; IEA.

GO; GO:0005098; P:viral genome replication; IEA.

R GO; GO:00190079; P:viral genome replication; IEA.
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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95.6%; Score 3027; DB 2; Length 303
Best Local Similarity 96.8%; Pred. No. 6.5e-227;
Matches 572; Conservative 9; Mismatches 10; Indels
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                                                                                                                                                                       InterPro; IPR001166; HCV RARP.
InterPro; IPR001650; HelTcase_C.
InterPro; IPR004109; Peptidase_S29.
InterPro; IPR0050319; Pept_Ser_Cys.
InterPro; IPR007095; RNA_pol_DS_PG.
InterPro; IPR007095; RNA_pol_DS_PG.
InterPro; IPR007094; RNA_pol_PSvir.
Pfam; PP01543; HCV capsid; 1.
Pfam; PP01542; HCV core; 1.
DEAD/DEAH N
HCV_capsid.
HCV_core.
                                                          HCV NS1.
HCV NS4a.
HCV NS4b.
HCV NS5a.
HCV RGRP.
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Pfam; PF01538; HCV NS; 1.
Pfam; PF0290; HCV NS; 1.
Pfam; PF02000; HCV NS4a; 1.
Pfam; PF01000; HCV NS4a; 1.
Pfam; PF01506; HCV NS5a; 1.
Pfam; PF01506; HCV NS5a; 1.
Pfam; PF001506; HCV NS5a; 1.
Pfam; PF001506; HCV NS5a; 1.
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IPR002531; H
IPR000745; H
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Bubmitted (NOV-1999) to the EMBL/GenBank databases.

Bubmitted (NOV-19
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
Q9J3H0, PRELIMINARY, PRT; 3010 AA. Q9J3H0; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Polyprotein.
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InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR0014145; DEAD./DEAM N.
InterPro; IPR001522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV core.
InterPro; IPR001490; HCV NS4a.
InterPro; IPR001490; HCV NS4b.
InterPro; IPR001490; HCV NS4b.
InterPro; IPR001409; Peptidase S29.
InterPro; IPR001409; Peptidase S29.
InterPro; IPR001409; Peptidase S29.
InterPro; IPR001409; Peptidase S29.
InterPro; IPR0017095; RNA POLIDS PF
INTERPRO; IPR001701; HCV NS4s; I.
IPR PF
INTERPROS PF
INTERP
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STRAIN=MDB-1;
MEDLINE=20013325; PubMed=10544098; DOI=10.1006/viro.1999.9924;
NAGGAyama K., Kurosaki M., Enomoto N., Mackawa S.y., Miyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                           Query Match 95.5%; Score 3026; DB 2; Length 3010; Best Local Similarity 96.3%; Pred. No. 7.8e-227; Matches 569; Conservative 14; Mismatches 8; Indels 0
3010 AA; 327098 MW; 737EEF31E3C2B28D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein.
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EMBL; AF165059; AAD56194.1; -
PIR; A61196; A61196.
PIR; PQ0246; PQ0246.
PIR; PQ0804; PQ0804.
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NCBI_TaxID=11103;
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MEDLINE=20013325; PubMed=10544098; DOI=10.1006/viro.1999.9924; Nagayama K., Kurosaki M., Enomico N., Mackawa S.y., Miyasaka Y., Tazawa J.i., Izumi N., Marumo F., Sato C.; Tazawa J.i., Izumi M. Marumo F., Sato C.; Tazawa Time-related changes in Full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0015021; C:integral to membrane; IEA.
R GO; GO:0019028; C:viral capsid; IEA.
R GO; GO:0019028; C:viral capsid; IEA.
R GO; GO:00019021; C:viral capeld; IEA.
GO; GO:000526; F:ATP-dependent helicase activity; IEA.
R GO; GO:0003723; F:RNA binding; IEA.
R GO; GO:0003958; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO:0005198; F:Rructural molecule activity; IEA.
R GO; GO:0005198; F:structural molecule activity; IEA.
R GO; GO:0005509; P:proteolysis and peptidolysis; IEA.
R GO; GO:0005509; P:transcription; IEA.
R GO; GO:0019097; P:viral genome replication; IEA.
R GO; GO:0019087; P:viral transformation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR011545; DEAD/DEAH N. InterPro; IPR001522; HCV capaid. InterPro; IPR002521; HCV core. InterPro; IPR002519; HCV-env. InterPro; IPR002511; HCV NS1. InterPro; IPR002511; HCV NS1. InterPro; IPR001490; HCV_NS4b.
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InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                           activity.";
Virology 263:244-253 (1999).
EMBL, AP165060; AAD56195.1; -.
PIR, A61196; A61196.
PIR; P00246; PQ0246.
PIR; P00854; PQ0234.
PIR; P00804; P00804.
PIR; PS0329; PS0329.
                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
  QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.5%; Score 3025; DB 2; Length 3010; Best Local Similarity 96.4%; Pred. No. 9.3e-227; Matches 570; Conservative 15; Mismatches 6; Indels 0
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2780 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLW 2839
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                                                                                                                             365 ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9QIX5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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protein;
                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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DR Pfam; PF01542; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
DR Pfam; PF01539; HCV core; 1.
DR Pfam; PF01530; HCV core; 1.
DR Pfam; PF01500; HCV NS1; 1.
DR Pfam; PF01000; HCV NS2; 1.
DR Pfam; PF01000; HCV NS4; 1.
DR Pfam; PF01001; HCV NS4; 1.
DR Pfam; PF00271; Hellcase C; 1.
DR Pfam; PF00297; Hellcase C; 1.
DR Pfam; PF0098; Viral Hellcase C; 1.
DR Pfam; PF0098; Viral Hellcase C; 1.
DR Pfam; PF00999; CTTOCHFONE C; 1.
DR Pfam; PF00999; Viral Hellcase C; 1.
DR Pfam; PF009999; Viral Hellcase C; 1.
DR Pfam; PF009999; Viral Hellcase C; 1.
DR Pfam; PF009999; VIII Hellcase C; 1.
DR Pfam; PF009999; VIII Hell
                                                                                                                                                                                                                                              Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases EMBL; D89872; BAA14035.1; -.
     P89966;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
RNA for polyprotein, complete cds.
                                                                                                                                                                                                                                                                                                                                                                             PIR, A61196, A61196.
PIR, PQ0246, PQ0246.
PIR, PQ0804, PQ0804.
PIR, PS0329, PS0329.
HSSP, Q81755, 1DXP.
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                            STRAIN=type 1b;
TANAKA T.;
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Tanaka T.;
         2900 EINRVASCLEKKLGVPPLKVWRHRARSVRAKCLSQGGRAATCGKYLFNWAVRTKLKLTPIP 2959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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llarity 96.4%; Pred. No. 1.1e-226;
Conservative 14; Mismatches 7; Indels 0
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InterPro; IPR002868; HCV_NS5a.
InterPro; IPR0012166; HCV_RGAP.
InterPro; IPR001650; Hellcase_C.
InterPro; IPR0040003; Peptidase_S29.
InterPro; IPR0040003; Peptidase_S29.
InterPro; IPR007003; Pept_U39_HCV_NS2.
InterPro; IPR0070095; RNA_DOI_DS_PS_C.
InterPro; IPR0070094; RNA_DOI_DS_PS_C.
Pfam; PF01543; HCV_Care; 1.
Pfam; PF01543; HCV_Care; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01509; HCV_NS1; 1.
Pfam; PF010006; HCV_NS2; 1.
Pfam; PF01001; HCV_NS2; 1.
Pfam; PF01001; HCV_NS4p; 1.
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570; Conserva
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95.4%; Score 3022; DB 2; Length 3010;

Query Match

PRT; 3010 AA

PRELIMINARY;

RESULT 12 P89966 ‡D P89966

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2424 SMSYTWTGALITPCAAEESKLPINPLSNSLLRHHNMIYATTSRSAGLROKKVTFDRLQVL 2483
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2604 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKSKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008026; F:ATP-dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003236; F:RNA binding; IEA.

GO; GO:0003236; F:RNA binding; IEA.

GO; GO:0005136; F:RETUCTURA MOLECULE activity; IEA.

GO; GO:0005136; F:RETUCTURA MOLECULE activity; IEA.

GO; GO:0005136; F:RETUCTURA MOLECULE activity; IEA.

GO; GO:0019079; P:PITANSCTIPTION; IEA.

GO; GO:0019079; P:VITAN GAME REPLIANTION; IEA.

R GO; GO:0019079; P:VITAN GAME REPLIANTION; IEA.

R INTERPO; IPRO0345; CYtC heme BS.

R INTERPO; IPRO03521; HCV_CORE.

R INTERPO; IPRO02519; HCV_CORE.

R INTERPO; IPRO03521; HCV_CORE.

R INTERPO; IPRO03521; HCV_NA4.

R INTERPO; IPRO0345; HCV_NA4.

R INTERPO; IPRO0346; HCV_NA5A.

R INTERPO; IPRO0346; HCV_NA5A.

R INTERPO; IPRO0366; HCV_NA5A.

R INTERPO; IRRO0409; PEPLICASE C.

R INTERPO; IPRO0409; PEPLICASE C.

R INTERPO; IPRO0409; PEPLICASE C.

R INTERPO; IRRO0409; PEPLICASE C.
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InterPro; IPR001656; Helicase C.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR004003; Pept Ser Cys.
InterPro; IPR007018; Pept Ser Cys.
InterPro; IPR007095; RNA_Dol_DS_PS.
InterPro; IPR007094; RNA_Dol_DS_PS.
InterPro; IPR01543; HCV_Core; 1.
IPR m; PF01550; HCV_NS1; 1.
IPR m; PF01006; HCV_NS2; 1.
IPR m; PF01006; HCV_NS4p; 1.
IPR m; PF01506; HC
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SEQUENCE 3(
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                      셤
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                                                                                                                                                                                                                                     65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
                                                                                                                                                                                                                                                                                                                                                                     SVWKDLLEDTDTP1QTTIMAKNEVFCVQPEKGGRKPARLIVPPDLGVRVCEKMALYDVVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCCDLAPBARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
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                                                                                                                                                2420 SMSYTWTGALITPCAAEESKLPINPLSNSLLRHHSMVYSTTSRSASLRQKKVTPDRLQVL
                                                                                                                                                                                                                                                                      2480 DDHYRDVLKEMKAKAKSTVKARLLSIEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
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                                                                                                               SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLROKKVTFDRLOVL
                                                    Gaps
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EMBL; AB04097; BB18180.1; -.
EMBL; A61196; A61196.
PIR; PS0329; PS0329.
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
Mishiro S.;
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                96.4%; Pred. No. 1.6e-226; indels :ive 12; Mismatches 9; Indels
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Last annotation update)
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MEROPS; S29.002; -.
G0; G0:0016021; C:integral to membrane; IEA.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0019031; C:viral envelope; IEA.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
             Local Similarity 96.4
les 570; Conservative
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NCBI_TaxID=11103;
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2660 QCCDLAPEAKLAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS 2719
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DR Pfam; PF01539; HCV_env; 1.

DR Pfam; PF01539; HCV_NS1; 1.

DR Pfam; PF01539; HCV_NS1; 1.

DR Pfam; PF02907; HCV_NS2; 1.

DR Pfam; PF01506; HCV NS4a; 1.

DR Pfam; PF01506; HCV NS4b; 1.

DR Pfam; PF00271; Hcll_Casc C; 1.

DR Pfam; PF00271; Hcll_Casc C; 1.

DR Pfam; PF00999; Viral_RARP; 1.

DR Pfam; PF00999; Viral_RARP; 1.

DR SWART; SN00487; DEXDC; 1.

DR SWART; SN00487; DEXDC; 1.

RW Coat protein; Bivelope protein; Glycoprotein; Monstructural protein; W Polyprotein; Transmembrane.

% SEQUENCE 3010 AA; 327266 ww.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.4%; Score 3021; DB 2; Length 3010; Best Local Similarity 96.3%; Pred. No. 1.9e-226; Matches 569; Conservative 14; Mismatches 8; Indels 0
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA-dependent RNA-polymerase (Fragment).
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                                                2784 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPIARAAWETARHTPVNSWLGNIIMYAPTLW 2843
                                                                                                                                                                                                                                                                                2904 EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGKYLFNWAVRTKLKLTPIP 2963
                                                                                                                                                                                          2844 ARMILMTHPFSILLVQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 2903
                                                                                                                                                                                                                                                   EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Genotype II/lb;
STRAIN=97170750; PubMed=9018054;
SUGIYAMA K., Kato N., Mizutani T., Ikeda M., Tanaka T., Shimotohno K.;
"Genetic analysis of the hepatitis C virus (HCV) genome from HCV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; BBRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                          infected human T colls.";

"General analygas of the nepatitis C virus (HCV) genome from HCV infected human T colls.";

J. Gen. Virol. 78:129-136 (1997).

EMBL, D8516; A61196.

R PIR, A61196; A61196.

R PIR, PQ0804; P00804.

R PIR, PQ0804; P00804.

R PIR, PQ0804; P00804.

R PIR, PQ0804; P00804.

R POS CO.0010021; C:integral to membrane; IEA.

GO; GO:0019026; C:viral capsid; IEA.

GO; GO:0019026; C:viral capsid; IEA.

GO; GO:000312; FiRNA binding; IEA.

GO; GO:0000312; FiRNA binding; IEA.

GO; GO:0000316; Firerine-type peptidase activity; IEA.

GO; GO:0000316; FiRNA binding; IEA.

GO; GO:0000317; FiRNA binding; IEA.

GO; GO:0000317; FiRNA binding; IEA.

GO; GO:0000318; FiRNA binding; IEA.

InterPro; IPR00140; HCV, NS4.

InterPro; IPR00140; PEQU GAS.

INTERPRO; IPR001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              009796;
01-JUL-1997 (TrEWBLrel. 04, Created)
01-JUL-1997 (TrEWBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Genomic RNA, complete cds.
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                                               Lohmann V., Korner F., Herian U., Bartenschlager R.,;

"Biochemical properties of hepatitis C virus NS5B RNA-dependent RNA polymerase and identification of amino acid sequence motifs essential for enzymatic activity.";

"J. virol. 71:8416-8428(1997).

REMBL: Z97730; CABIO747.1, -

REMBL: Z97730; CABIO747.1, -

REMBL: MHU; X-ray; A/B=1-570.

RO; GO:0005224; F:ATP binding; IEA.

GO; GO:0003568; F:RNA binding; IEA.

GO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.

RO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.

RO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.

RO; GO:0004569; F:RNA-directed RNA polymerase activity; IEA.

RO; GO:0019799; P:Viral genome replication; IEA.

RITERPRO; IPR007095; RNA_pol_DS_FS.

InterPro; IPR007095; RNA_pol_DS_FS.

InterPro; IPR007099; Viral RARP; 1.
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                                    MEDLINE=98001363; PubMed=9343198;
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Sequence 12, Appl
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Sequence 6, Appli
Sequence 15, Appli
Sequence 3, Appli
Sequence 27, Appli
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Sequence 33, Appli
Sequence 33, Appli
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Batent No. 6383768

GENERAL INFORMATION:
APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: DEMERANCESCO, Raffaele
APPLICANT: DEMERANCESCO, Raffaele
APPLICANT: DEMERANCESCO, Raffaele
APPLICANT: DEMERANCE Licia
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
TITLE OF INVENTION: POLYMERASE AND TERMINAL NUCLECTIDYL TRANSFERASE
TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILE REFERENCE: 170002P
CURRENT APPLICATION NUMBER: US/08/952,981A
CURRENT PAPLICATION NUMBER: 1998-03-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1
SEQ IN 1
SEQ ID NO 1

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US-09-539-601-9
US-09-539-601-12
US-09-539-601-24
US-09-539-601-15
US-09-539-601-13
US-09-539-601-3
US-09-539-601-18
US-09-539-601-18
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US-09-59-601-33
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US-09-59-601-33
US-09-59-801-33
US-09-119-41-908-11
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ELITSCSSNVSVAHDASCKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
                  361 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAMETARHTPVNSWLGNIMYAPTLW
                                                                                                                                      EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLTPIP
                                                                                                                                                                                                       APPLICANT: CANYAMA, HITOTO
APPLICANT: FUKE, ISAO
APPLICANT: FUKE, ISAO
APPLICANT: MORI, Chisato
APPLICANT: YOSHIDA, IWAO
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/34,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-167466
FILING DATE: 25-UNA-1900
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-30201
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-305605
FILING DATE: 30-UUL-1993
PRIOR APPLICATION NAMBER: US 08/099,706
FILING DATE: 30-UUL-1993
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/69,996
FILING DATE: 28-DEC-1990
ATTORNEY ASCI-1991
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY ASCIITATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY ASCIITATION UNMBER: S0-0000331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 900703D TELECOMMUNICATION: TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                         Sequence 50, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
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TELEX: 440142
INFORMATION FOR SEQ ID NO:
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STATE: D.C.
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Sequence 50, Application US/08384616;
Patent No. 584701

GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: TUKE, Isao
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES: ATMETORY, Westerman, Hattori, McLeland & ADDRESSES: Armstrong, Westerman, Hattori, McLeland & STREET: 1725 K St. N.W. Suite 1000
CITY: Wasshington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                              ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
                                                                                                                                                             Query Match

95.2%; Score 3016; DB 1; Length 997;
Best Local Similarity 96.6%; Pred. No. 4.8e-298;
Matches 571; Conservative 11; Mismatches 9; Indels
; SEQUENCE CHARACTERISTICS:
; LENGTH: 997 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-324-977-50
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827 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 886
                                                                                                                                              545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 595
                                                                                                                                                                      947 AASRLDISGWFVAGYSGGDIYHSISRARPRWFMLCLLLLSVGVGIYLLPNR 997
                                                                                                                                                                                                                                                           APPLICANT: OKAYAWA, HIROTO

APPLICANT: FUKE, ISAO

APPLICANT: TAKANIZAWA, Akahisa

APPLICANT: TAKANIZAWA, Akahisa

APPLICANT: TAKANIZAWA, Akahisa

APPLICANT: TAKANIZAWA, Akahisa

APPLICANT: YOSHIDA, IWAO

TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC

TITLE OF INVENTION: ONA AND ANTIGEN POLYPEPTIDE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSE: Armatrong, Westerman, Hattori, McLeland & STREE: 1725 K St. N.W. Suite 1000

CITY: Washington

STATE: D.C.

COUNTRY: U.S.

ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOPTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
FILING DATE: 18-OCT-1994
FILING DATE: 25-JUN 1990
FILING DATE: 31-AUG-1990
FILING DATE: 31-AUG-1990
FILING DATE: 31-AUG-1990
FILING DATE: 31-AUG-1990
FILING DATE: 09-NOV-1990
FILING DATE: 30-JUL-1993
FILING DATE: 30-JUL-1993
FILING DATE: 30-JUL-1993
FILING DATE: 02-OCT-1991
FILING DATE: 02-OCT-1991
FILING DATE: 26-DEC-1991
FILING DATE: 28-DEC-1991
FILING DATE: 28-DEC-1990
ATTONNEY, AGENT TIRFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INPORMATION:
TELEPRAX: (202) 887-0357
INPORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 997 amino acids
TYPE: amino acids
TOPOLOGY: linear
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95.2%; Score 3016; DB 2; Length 997;
Best Local Similarity 96.6%; Pred. No. 4.8e-298;
Matches 571; Conservative 11; Mismatches 9; Indels (
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                           CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 0.2-CT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-UIN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: JP 2-305605
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M. REGISTAATION NUMBER: 36,281
REFERRENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
                                                                        SUFTWARE: ASCII.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 659-2930
(202) 887-0357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 997 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                        407 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNWYYATTSRSAGLRQKKVTFDRLQVL 466
                                                                                                                                                                DDHYRDVLKEMKAKASTVKAKLLSVERACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                244
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                                                                                                                                                                                                                                                                                                                                                             AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLW 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCCDLAPEARQAIRSLTERLYVGGPMTNSKGONCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                                                                                                                                                                                                                                                                                                                        AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                          SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                    TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                       5 SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLRQKKVTFDRLQVL
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/09315850;
Patent No. 621787;
GENERAL INFORMATION:
APPLICANT: FURE, Isao
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
CORRESPONDENCES: 50
CORRESPONDENCES: 50
CORRESPERSEE: AMBRICON, Westerman, Hattori, McLeland & ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & CITY: Washington
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
CCUNTY: VASAINGTON
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                                            Length 997;
                                                                          9; Indels
                                         95.2%; Score 3016; DB 2; 96.6%; Pred. No. 4.8e-298; tive 11; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                          Best Local Similarity 96.6
Matches 571; Conservative
; MOLECULE TYPE: protein US-08-904-686A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20006
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BLITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 OCCDLAPRARQAIRSLITERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLITCYLKAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVWKDILLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 AACRAAKLODCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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95.2%; Score 3016; DB 3; Length 997;
Best Local Similarity 96.6%; Pred. No. 4.8e-298;
Matches 571; Conservative 11; Mismatches 9; Indels
                                                                                                                                 PRIOR APPLICATION DATA;
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA;
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA;
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA;
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 07/69,996
FILING DATE: 28-DEC-1990
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLELBING LE-Nhung
REGISTRATION NUMBER: 31,541
REFERENCEY/DOCKET NUMBER: 31,541
REGULANDER: COCKET NUMBER: 31,541
REGULANDER: COCKET NUMBER: 31,541
REGULANDER: COCKET NUMBER: 31,541
REGULANDER: COCKET NUMBER: 31,541
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
FILING DATE:
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Query Match
Best Local Similarity
                                                                                                                                                      RESULT 7
US-08-324-977-36
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SEQUENCE 2, Application US/08952981A
Fatent No. 638368
GENERAL INFORMATION:
APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: DE FRANCESCO, Raffaele
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
ELENGTH: 2201
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65 DDHYRDVLKEMKAKASTVKAKLLSVERACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
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; ORGANISM: cDNA clone pCD (38-9.4)
US-08-952-981A-2
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Best Local Similarity 96.6
Matches 571; Conservative
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US-08-952-981A-2
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MOLECULE TYPE: protein
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                                                      2031 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNWYATTSRSAGLRQKKVTFDRLQVL 2090
                                                                                                                              2091 DDHYRDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIH 2150
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                                                                                                          65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
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                                   5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL 64
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Fatent No. 5847101
GENERAL INFORMATION:
APPLICANT: CKAYAMA, Hiroto
APPLICANT: FUKE, Laao
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZOWA, Akahisa
APPLICANT: TAKAMIZOWA, Akahisa
APPLICANT: TAKAMIZOWA, Akahisa
APPLICANT: TAKAMIZOWA, Akahisa
APPLICANT: AMSTONO; Westerman, Hattori, McLeland & ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & CITY: Washington
CITY: Washington
9; Indels
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MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOPTWARE: ASCII
 11; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
FILING DATE:
CLASSIFICATION: 424
 571; Conservative
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STATE: D.C.
COUNTRY: U.
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2151 SVWKDLLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2210
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PRICE AT STATEMENT OF THE STATEMENT OF T
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TELEX: 440142
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2621 amino acids
TYPE: amino acid
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TELEFAX: (202) 887-0357
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                   US-08-904-686A-36

Sequence 36, Application US/08904686A

Sequence 36, Application US/08904686A

Sequence 36, Application US/08904686A

SEQUENCE 36, SEQUENCE 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: JD 2-167466
FILING DATE: 25-JUN 1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCCLeland, Le-Muning
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 31,541
TELEPHONE: (202) 659-2930
TELEPHONE: (202) 659-2930
TELEPRAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 36:
SERGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 2621 amino acids
amino acid
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Best Local Similarity 96.6
Matches 571; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20006
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2091 DDHYRDVLKEMKAKASTVKAKTLSVEBACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIH 2150
                                                                                                                                                                                                           2151 SVWKDLLEDTVTFIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2210
2031 SMSYTWTGALITPCAABESKLPINALSNSLLRHHNMVYATTSRSAGLROKKVTFDRLQVL 2090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2331 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPRYDL 2390
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                                                                                                                                                                                                                                                                                                                                                                                                                   245 QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2271 QCCDLAPEARQAIKSLIERLYIGGPLINSKGQNCGYRRCRASGVLITSCGNTLICYLKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2391 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLTPIP
                                                                                                                                                                            125 SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                                   185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTĽW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2571 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 2621
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Sequence 36, Application US/09315850

Patent No. 6217872

Patent No. 6217872

APPLICANT: PUKE, Isaco

APPLICANT: PUKE, Isaco

APPLICANT: TAKAMIZAWA, Akahisa

APPLICANT: TOSHIDA, Iwao

TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC

TITLE OF INVENTION: DNA AND ANTIGEN POLYPEPTIDE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSER: Amaghton

ADDRESSER: Naughton

ADDRESSER: Naughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSER: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-040-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
FILING DATE:
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2571 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 2621
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              545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Naughton Westerman, Hattori, McLeland & ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000
CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: OSSYTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                      APPLICANT: OCKAYAWA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TARANIZAMA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.6%; Pred. No. 3e-29
Matches 571; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REGISTRATION NUMBER: 36,281
RECISTRATION NUMBER: 36,281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
                                                                                                                                                                                             Sequence 2, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3010 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                             RESULT 11
US-08-324-977-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2031 SMSYTWTGALITPCAAEESKIPINALSNSLLRHHNWYYATTSRSAGLRQKKVTFDRLQVL 2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2091 DDHYRDVLKEMKAKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIH 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2151 SVWKDLLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2211 TLPQVVMGSSYGFQYSPGQRVEFLVNTWKSKKNPMGFSYDTRCFDSTVTENDIRVEESIY 2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2331 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2391 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIMYAPTLW 2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAPSLHSYSPG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACRAAKLODCTWLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.2%; Score 3016; DB 3; 96.6%; Pred. No. 2.4e-297; tive 11; Mismatches 9;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-0701-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-A0G-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: McLeland, Le-Nhung
REGISTRATION NOMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 659-2930
TELEPAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2621 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 96.64
Matches 571; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-09-315-850-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485
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ö 5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL 64 Gaps °,

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2420 SMSYTWTGALITPCAAEESKLPINALGNSLLRHHNNVYATTSRSAGLRQKKVTFDRLQVL 2479
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                                                                                                                                       | SVWKDLLEDTDTPIQTTIMAKNEVPCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                              DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                                                                                                                               QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
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                                                                                                                                                                                                                  TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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APPLICANT: OKAYAWA, Hiroto
APPLICANT: PUKE, 18ac
APPLICANT: PUKE, 18ac
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: ONNA AND ANTIGEN POLYPEPTIDE
CORRESPONDENCE ADDRESS:
ADDRESSEE AMBELTONG, Westerman, Hattori, McLeland & ADDRESSEE Amaghton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-UTN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08324977
Patent No. 5747339
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US-08-324-977-14
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2900 EINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLPNWAVKTKLKLTPIP 2959
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APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
RIOR APPLICATION DATE:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/65,451
FILING DATE: 28-DEC-1990
ATTORNEY AGENT INFORMATION:
NAMB: Stevens-Smith, Theres M.
REGISTRATION NUMBER: 36,281
REPERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 440142
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3010 amino acids
TYPE: amino acid
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125 SVWKDLLEDTDTF1QTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-0CT-1991
APPLICATION NUMBER: US 016466
FILING DATE: 25-UN-1990
PRIOR APPLICATION DATA:
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
FILING DATE: 31-AUG-1990
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; Sequence 14, Application US/08384616
; Sequence 10. Application
; GENERAL INFORMATION:
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                                                      Sequence 2, Application US/08384616;
Patent No. 5847101
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PUKE, ISAO
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
ITILE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
ITILE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.2%; Score 3016; DB 2; Length 3010; 96.6%; Pred. No. 3e-297; tive 11; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: Naughton ADDRESSEE: 1725 K St. N.W. Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDAER: 07/769,996
FILING DATE: 02-0CT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-0TM-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-A0G-1990
PRIOR APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-0V-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 28-DEC-1990
ATTORNEY AGENT INCRMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 36,281
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 36,281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
FILING DATE:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3010 amino acids
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Best Local Similarity
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COUNTRY: U
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STREET: 1
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                                                                                           185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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APPLICANT: FUKE, 18a0
APPLICANT: FUKE, 18a0
APPLICANT: MORI, Chisato
APPLICANT: MORI, Chisato
APPLICANT: MORI, Chisato
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: DONA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPED ALMSTRONG, Westerman, Hattori, McLeland &
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
CITY: Washington
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STRATE: D.C.
CCUNTRY: U.S.A.
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ZIP: 20006

COMPUTER READBLE FORM:

MEDLIUM TYPE: Diskette, 3.5 in, 1.44Mb

COMPUTER: IBM PC compatible

COMPUTER: ISM PC COMPATIBLE

CORFERATE: PC-DOS/NS-DOS, Version 5.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2660 QCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS 2719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
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         PRION APPLICATION DATA:
PILLING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INPORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAK: (202) 887-0357
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
                                                                                                                                                                                                                                         TELEFAX: (202) 887-0357
TELEX: 440142
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3010 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.6
Matches 571; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-384-616-14
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Sequence 2, Application US/08904686A Patent No. 5998130 GENERAL INFORMATION: APPLICANT: CASYAMA, Hiroto APPLICANT: FUKE, 18ao

US-08-904-686A-2

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2420 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNWYYATTSRSAGLRQKKVTFDRLQVL 2479
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APPLICANT: MORI Chisato
APPLICANT: TAKANIZANA, Akahisa
APPLICANT: TAKANIZANA, Akahisa
APPLICANT: YASHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000 CITY: Washington STATE: D.S.A.
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
PRICATION DATA:
PRICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-CCT-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: JF 2-167466
FILING DATE: 25-JUN-1990
PRICA APPLICATION DATA:
APPLICATION NUMBER: JF 2-230921
FILING DATE: 31-AUG-1990
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRICA APPLICATION DATA:
APPLICATION DATA: BAPPLICATION DATA:
PRICING DATE: 30-JUL-1993
PRICA APPLICATION DATA: US 07/69,996
FILING DATE: 02-OCT-1991
PRICA APPLICATION DATA: US 07/635,451
FILING DATE: 28-DEC-1990
ATTIONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENGE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEBRONE: (202) 887-0357
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3010 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-904-686A-2
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TOPOLOGY: linear
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YDTRCFDSTVTENDIRVEESIY 244		FTEAMTRYSAPPGDPPODEYDL 364	TARHTPVNSWLGNIMYAPTLW 424	LPQIIERLHGLSAFSLHSYSPG 484 LPQIIERLHGLSAFSLHSYSPG 2899	AICGKYLFNWAVRTKLKLTPIP 544 ATCGKYLFNWAVKTKLKLTPIP 2959	LSVGVGIYILPNR 595 LSVGVGIYILPNR 3010	
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Search completed: September 22, 2005, 14:47:44 Job time : 30 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 6, Appli
Sequence 1, Appli
                                                                                    (without alignments)
3218.609 Million cell updates/sec
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                                                                                                                                                                                                                                  1 MASMSWSYTWTGALITPCAA.....LLSVGVGIYLLPNRHHHHH 601
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                                                      September 22, 2005, 14:43:14; Search time 76 Seconds
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1. /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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S US-10-712-479-4

US-10-085-476-1

US-10-085-476-2

US-10-492-178-6

S US-10-492-178-6

US-10-471-164-5

US-09-898-297-1

US-10-238-282-1

US-10-238-259A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*
OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                           Scoring table:
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                                                         Run on:
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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appl Sequence 6, Appli Sequence 6, Appli	Sequence 42, Appl Sequence 42, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 14, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 2, Appli	Sequence 406, App Sequence 4, Appli Sequence 9, Appli Sequence 20, Appl
15 US-10-198-384A-1 16 US-10-471-164-1 16 US-10-851-710-1 9 US-09-838-386-12 16 US-10-471-164-6 9 US-09-742-659-6	16 US-10-259-275-42 17 US-10-259-275-42 20 US-11-006-313-42 18 US-10-029-907-3 19 US-10-109-561-3 16 US-10-10-10-11 16 US-10-686-835-3 16 US-10-686-835-3 16 US-10-686-835-3 16 US-10-492-178-1 17 US-10-241-872-12 18 US-10-241-872-12 19 US-10-241-949-15 10 US-09-194-949-15 11 US-10-614-31-15 12 US-10-211-455-2 13 US-10-211-455-4 14 US-10-211-455-4 16 US-10-211-455-4 17 US-10-211-455-4 18 US-10-211-455-4 19 US-10-313-13-13	-10-296-734- 09-742-659-4 09-952-572-9 09-747-419-2
621 621 621 627 627 2865	11998 2229888 322201 322201 322201 3229885 3240 5240 5240 5240 5240 5240 5240 5240 5	
95.1 95.1 1.29 95.1 1.69	4 4 4 4 4 4 4 4 4 4 4 4 4 6 9 9 9 9 9 9	87.7 87.6 87.6 87.6
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ALIGNMENTS

```
### SEQUENCE 2, Application US/10712479

### SEQUENCE 3, Application US/20303031

### SEPLICANT: Wells, Peter A.

### APPLICANT: Beps Dennis E.

### CURRENT APPLICANTON: Activity 100.04; Score 3167; DB 16; Length 601;

### APPLICANT: Beps Dennis E.

### APPLICANT: Beps Dennis
```

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Sequence 1, Application US/10085476

Sequence 1, Application US/10085476

Publication No. US20020164722A1

GENERAL INFORMATION:

APPLICANT: De Francesco, Raffaele
APPLICANT: Tomei, Licia
APPLICANT: Tomei, Licia
TITLE OF INVENTION: MENA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL
TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILE REFERENCE: 170022AA
CURRENT APPLICATION NUMBER: US/10/085,476
CURRENT PILING DATE: 1996-05-29
PRIOR PLING DATE: 1996-05-24
PRIOR PLING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: RM95A000343
PRIOR PLING DATE: 1995-05-25
NUMBER OF SEQ ID NOS: 14

SOFTWARE FRENCE: RESERVED

SOFTWARE FRENCE: NOS: 14
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                     181 DVVSTLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVE
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Best Local Similarity 96.6%; Pred. No. 2.5e-266;
Matches 571; Conservative 11; Mismatches 9;
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Fublication No. US20040209283A1

GENERAL INFORMATION:

APPLICANT: Sheets, Michael P.

APPLICANT: Sheets, Michael P.

APPLICANT: Wells, Peter A.

APPLICANT: Wells, Poorman, Roger A.

APPLICANT: Bpps, Dennis E.

APPLICANT: Bpps, Dennis E.

TITLE OF INVENTION: Accitius A.

TITLE OF INVENTION: Ac
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                                             NHIRSVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALY 180
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ORGANISM: Artificial
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US-10-712-479-4
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65 DDHYRDVLKEMKAKASTVKAKLLSVEBACKU TPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
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                     305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
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   5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLROKKVTFDRLQVL
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TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA Replicase
FILE REFERENCE: 76-95C
CURRENT APPLICATION NUMBER: US/10/241,872
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: 09/597,877
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 1995-09-27
PRIOR FILING DATE: 1996-09-27
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2151 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR 2201
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Best Local Similarity 96.3%; Pred. No. 3.8e-266;
Matches 569; Conservative 12; Mismatches 10;
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LENGTH: 593
TYPE: PRT
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APPLICANT: De Francesco, Raffaele
APPLICANT: De Francesco, Raffaele
APPLICANT: Tomei, Licia
APPLICANT: Tomei, Licia
APPLICANT: De Francesco, Raffaele
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
TITLE OF INVENTION THANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILE REFERENCE: 10002-02-27
CURRENT APPLICATION NUMBER: 08/952,981
PRIOR PELING DATE: 1996-03-23
PRIOR PELING DATE: 1996-03-24
PRIOR PILING DATE: 1996-03-24
PRIOR FILING DATE: 1995-05-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2201
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                                                                         TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
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SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL 64
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; Publication No. US20020164722A1
; GENERAL INFORMATION:
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ORGANISM: HCV
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                                                                                                                               123 SVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 182
                                                                                                                                                                                                                                                                              305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
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                                      DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                            SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
SMSYTWTGALITPCAAEEQKLPINALSNSLLRHHNMVYATTSRSASLRQKKVTFDRLQVL 62
                                                                                                                                                                                   TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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Subjication No. US20040247615A1

Subjication No. US20040247615A1

Subjication No. US20040247615A1

Subjication No. US20040247615A1

APPLICANT: Emini, Emilio A.

APPLICANT: Shiver, John W.

APPLICANT: Labm, Armin

APPLICANT: Luzzago, Alessandra

APPLICANT: Lorese, Riccardo

APPLICANT: Cortese, Riccardo

APPLICANT: NUMBER: Cortese

FURBENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: 60/363,774

PRIOR APPLICATION NUMBER: 60/363,774

PRIOR PILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 60/363,774

PRIOR PILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 1985
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ORGANISM: Artificial Sequence
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US-10-492-178-6
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Sequence 5, Application US/10471164

Publication No. US20040110126A1

GENERAL INFORMATION:

TITLE OF INVENTION: HCV POLYMERASE INHIBITOR ASSAY

FILE REFERRINGE: 13/094

CURRENT APPLICATION NUMBER: US/10/471,164

CURRENT PILING DATE: 2003-09-05

PRIOR PILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: SPIT
Query Match 95.1%; Score 3012; DB 16; Best Local Similarity 96.4%; Pred. No. 3.4e-265; Matches 570; Conservative 12; Mismatches 9;
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184

244 270 304 364 390 424 450 484 544

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91 DDHYRDVLKEMKAKASTVKAKALLSVERACKLTPPHSAKSKFGYGAKDVRNLSSKAVDHIR 150
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                        151 SVWKDLLEDTETPIDTTIMAKNEVFCVOPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                       185 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                          211 TLPQAVMGSSYGFQXSPKQRVEFLVNAWKSKKCPMGFSYDTRCFDSTVTESDIRVEESIY
                                                                                                                                       QCCDLAPEARQAIRSLTERLYVGGPWTNSKGONCGYRRCRASGVLTTSCGNTLTCYLKAA
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Publication No. US20030176433A1
GENERAL INFORMATION:
APPLICATION NO. US20030176433A1
GENERAL INFORMATION:
TITLE OF INVENTION: Viral Polymerase Inhibitors
FILE REPERENCE: 13/095
CURRENT FILING DATE: 2002-07-18
FRICH APPLICATION NUMBER: 60/338,061
FRICH APPLICATION NUMBER: 60/338,061
FRICH APPLICATION NUMBER: 60/336,061
FRICH APPLICATION NUMBER: 60/336,061
FRICH APPLICATION NUMBER: 60/336,061
FRICH APPLICATION NUMBER: 60/336,061
FRICH APPLICATION NUMBER: 60/307,674
FRICH FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE PEASES FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.1%; Score 3011; DB 14;
Best Local Similarity 95.9%; Pred. No. 7.6e-266;
Matches 567; Conservative 18; Mismatches 6;
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US-10-198-680A-1
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                                                                  TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILLE OF INVENTION: VIRAL POLYMERASE INHIBITORS;
TITLE OF INVENTION: VIRAL POLYMERASE INHIBITORS;
FILLE REPREBACE: 13/079
CURRENT APPLICATION NUMBER: US/09/898,297
CURRENT PILING DATE: 2001-07-03
FRIOR PILING DATE: 2000-07-06
FRIOR PILING DATE: 2000-07-06
FRIOR FILING DATE: 2001-03-08
FRIOR FILING DATE: 2001-03-08
FRIOR FILING DATE: 2001-04-02
FRIOR PILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020065418A1
GENERAL INFORMATION:
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   271 QCCDLAPEARQAIKSLTERLYIGGPLTNSKGONCGYRRCRASGVLTTSCGNTLTCYLKAS 330
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Publication No. US2030236251A1
GENERAL INFORMATION:
THE PERFECT INFORMATION:
TITLE OF INVENTION: Viral Polymerase Inhibitors
FILE REFERENCE: 13/089
CURRENT APPLICATION NUMBER: US/10/198,259A
CURRENT FILING DATE: 2002-07-18
FRIOR PRILING DATE: 2001-07-20
FRIOR PELLING DATE: 2001-07-20
FRIOR PILING DATE: 2001-07-20
FRIOR PILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PARTSEQ for Windows Version 4.0
SSOFTWARE: 63
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Best Local Similarity 95.9%; Pred. No. 7.6e-266;
Matches 567; Conservative 18; Mismatches 6;
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ORGANISM: HCV NS5B
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                                   QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                      AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
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US-10-238-282-1

Sequence 1, Application US/10238282

PUDICATION NO. US20030232816A1

GENERAL INFORMATION:

TITLE OF INVERTION:

TITLE OF INVERTION:

CURRENT APPLICATION NUMBER: US/10/238,282

CURRENT APPLICATION NUMBER: US/10/238,282

CURRENT APPLICATION NUMBER: 60/216,084

PRIOR APPLICATION NUMBER: 60/216,084

PRIOR PILING DATE: 2000-07-06

PRIOR APPLICATION NUMBER: 60/274,374

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-04-02

NUMBER OF SEQ ID NOS: 1

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 1.

LENGTH.
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; ORGANISM: Hepatitis C Virus
US-10-238-282-1
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JOS-10196-3594A

Publication No. US20040024190A1

GENERAL INFORMATION:

APPLICANT: Bochtinger Ingelheim (Canada) Ltd.

TITLE OF INVENTION: Viral Polymerase inhibitors

FILE REFERENCE: 13/090

CURRENT APPLICATION NUMBER: US/10/198,384A

CURRENT PILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/338,061

PRIOR APPLICATION NUMBER: 60/307,674

PRIOR APPLICATION NUMBER: 60/307,674

PRIOR APPLING DATE: 2001-07-25

NUMBER OF SEQ ID NOS: 4

SEQTIANG: PASESEQ for Windows Version 4.0

SEQTIANGTH: 621
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: HCV NS5B
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US-10-198-384A-1
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510 124 150 184 210 244 270 304 330 364 390 424 450 484 510 544 570 64 90 EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGKYLFNWAVRTKLTPIP 31 SMSYTWIGALITPCAAEESQLPINALSNSLVRHRNMVYSTISRSAALRQKKVIFDRLQVL 65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 91 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVDHIR 125 SVWKDLLEDTDTPIQTTIMAKNBVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 211 TLPQAVMGSSYGFQYSFKQRVEFLVNAWKSKKCPMGFSYDTRCFDSTVTESDIRVEESIY QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 271 QCCDLAPEARQAIKSLIERLYIGGPLINSKGQNCGYRRCRASGVLITSCGNTLICYLKAS 391 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAWETARHTPINSWLGNIMYAPTLW ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 451 ARMVLMTHFPSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLROKKVTFDRLQVL Gaps 545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRWFWLCLLLLSVGVGIYLLPNR 595 ö Length Indele RESULT 13
US-10-471-164-1
; Sequence 1, Application US/10471164
; Publication No. US20040110126A1
; GENERAL INFORMATION:
; APPLICANT: George KUKOLJ and Ginette MCKERCHER
; TITLE OF INVENTION: HCV POLYMERASE INHIBITOR ASSAY.
; FILE REPERENCE: 13/094
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/274,374
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 621 Query Match 95.1%; Score 3011; DB 16; Best Local Similarity 95.9%; Pred. No. 7.6e-266; Matches 567; Conservative 18; Mismatches 6;

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Search completed: September 22, 2005, 14:49:31 Job time: 79 secs
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571 AASRLDLSGWFVAGYNGGDIYHSLSRARPRWFMLCLLLLSVGVGIYLLPNR
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95.9%; Pred. No. 7.6e-266;
tive 18; Mismatches 6;
                                                                                                                                 GENERAL INFORMATION:

APPLICANTE BOGHRINGER INCELHEIM (CANADA) LTD.

TITLE OF INVENTION: VIRAL POLYMERASE INHIBITORS
FILE REFERENCE: 13/079

CURRENT APPLICATION NUMBER: US/10/851,710

CURRENT FILING DATE: 2004-05-21

PRIOR APPLICATION NUMBER: US/10/238,282

PRIOR APPLICATION NUMBER: 60/216,084

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2001-07-08

PRIOR FILING DATE: 2001-07-08

PRIOR FILING DATE: 2001-04-02

NUMBER OF SEQ ID NOS: 1

SOFTWARE FRASESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: EMBITHER
                                                                                      Sequence 1, Application US/10851710
Publication No. US20040224955A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT

ORGANISM: Hepatitis C Virus

US-10-851-710-1
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Best Local Similarity 95.9%
Matches 567; Conservative
                                                                                                                          GENERAL INFORMATION:
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Sequence 12, Application US/09838386

Patent No. US20010055756A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Pellerin. Charles

APPLICANT: Pellerin. Charles

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

CURRENT APPLICATION NUMBER: US/09/838,386

CURRENT APPLICATION NUMBER: US 60/198,793

PRIOR PILING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.0

SEQ ID NO 12

LENGTH: 627
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9
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95.1%; Score 3011; DB 9;
Best Local Similarity 95.9%; Pred. No. 7.7e-266;
Matches 567; Conservative 18; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: HTAA5B polymerase
US-09-838-386-12
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ORGANISM: Artificial Sequence
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WPI; 2004-420337/39.
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                         geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
                                                                                                                                                                                                                                A_Geneseq_16Dec04:*
.: geneseqp1980s:*
: geneseqp1990s:*
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Match Length DB
                                                                               US-10-712-479-4
       Copyright
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seq length: 585
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Perfect
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Maximum I
                                                Run on:
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Abw01861 HCV-CKS-N	ABW01861	7	496	36.8		45
	AAB51375	4	496	36.8	1124	44
Aar33577 HCV CKS-N	AAR33577	~	496	36.8		43
7 HCV (AAR33597	0	496	36.8		42
_	AAR33635	~	496	36.8		41
Aar21568 HCV CKS-1	AAR21568	~	496	37.0		40
Aaw41751 Hepatiti	AAW41751	~	224	37.8		39
Aar25873 HCV poly	AAR25873	0	224	37.8		38
Aar25895 HK20. 9/	AAR25895	0	251	37.9	1158.5	37
Aar25891 HK16. 9/	AAR25891	0	253	38.5		36
Aaw41747 Hepatitis	AAW41747	0	239	38.5		35
Aar25869 HCV poly	AAR25869	~	239	38.5		34
Aaw41752 Hepatiti	AAW41752	~	247	38.5		33
Aar25874 HCV polyn	AAR25874	~	247	38.5		32
	AAR25896	~	270	38.6		31
Abb77285 HCV bait	ABB77285	Ŋ	260	40.3	1232	30
	AAR29879	0	,582	44.6		29
'n	AAR38285	N	365	45.0		28
Aar38286 NANB hepa	AAR38286	~	365	45.3	1384	27
Aar38287 NANB hepa	AAR38287	~	365	45.5		56

ALIGNMENTS

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Hepatitis C virus infection; HCV infection; polymerase; NS5B; bone mineral disease; osteoporosis; carcinoma; cardiovascular disease; diabetes; ocular disorder; renal dysfunction; lymphoma; lymphopoliferative disorder; metabolic disorder; arthritis; sleep disorder; thyroid disorder; antiniflammatory; hepatotropic; virucide; osteopathic; cycostatic; antiniflammatory; hepatotropic; nephrotropic; antiathritic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting RNA polymerase activity in a continuous-read manner, useful treating osteoporosis, carcinomas, cardiovascular diseases, ocular disorders or arthritis, by contacting an RNA polymerase with an oligonucleotide template.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE;
                                                                                                                                                                                                                                              C-terminally truncated HCV NS5B polymerase, Cdelta21 NS5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheets MP, Wells PA, Shelly JA, Poorman RA,
                                                                                                                                                                                                                                                                                                                               polymerase activity; continuous-read assay;
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ADO19023 standard; protein; 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2002; 2002US-0425981P.
                                                                                                                                                                  (first entry)
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claim 7; SEQ ID NO 4; 46pp; English.

in

The present invention relates to a method for detecting RNA polymerase estivity in a continuous-read manner. The method comprises contacting an RNA polymerase with an oligomucleotide template in a reaction mixture comprising an assay buffer, under conditions in which the RNA polymerase

13-NOV-2002

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is active, adding a fluorescent dye capable of binding double-stranded nucleic acid molecules to the reaction mixture, and measuring the fluorescence of the reaction mixture. The RNA polymerase is the Hepatitis C virus (HCV) polymerase, NSSB. The method is useful for treating HCV infection, bone mineral diseases like osteoporosis, carcinomas, cardiovascular diseases, diabetes, ocular disorders, renal dysfunction, lymphomas, lymphopoliferative disorders, metabolic disorders, arthritis, sleep disorders and thyroid disorders. The present sequence represents C terminally truncated HCV NSSB polymerase (designated Cdelta21 NSSB).
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                                                                                                                                                                                                                                                                                                                                                  NHIRSVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESIYOCCDLAPEARQAIRSLTERLYVGGPMTNSKGONCGYRRCRASGVLTTSCGNTLTCY
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                                                                                                                                                                             580;
                                                                                                                                                                          100.0%; Score 3055; DB 8; Length 100.0%; Pred. No. 7e-285; ive 0; Mismatches 0; Indels
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Best Local Similarity
Matches 580; Conserv
                                                                                                                                                Sequence 580 AA;
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Antiviral; hepatitis C virus; HCV; NS5B RNA polymerase.

Unidentified EP1256628-A2

Mutant RNA polymerase MUT-2 protein

30-JAN-2003

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The invention relates to an isolated, purified nucleic acid molecule, which encodes a mutant hepatitis C virus (HCV) NS5B RNA polymerase, where a point mutation occurs at least at one or all of positions 47, 101, 106, and/or 114 of the native RNA polymerase sequence not defined in the specification. The method of the invention is utilised to identify inhibitors of the polymerase. The inhibitors serving as lead compounds for the design of potentially therapeutic compounds for the treatment of HCV. The mutant HCV NS5B RNA polymerase has improved crystallisation properties as compared to a native HCV NS5B RNA polymerase. This sequence represents a mutant RNA polymerase protein of the invention. NOTE: This sequence is not shown in the specification. It is, however, described in the specification and its sequence has been obtained from an electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDHYRDVLKEMRAKASTVKAKILISVERACKLTPPHSAKSKFGYGAKDVRNLSSRAVNHIH 120
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                                                                                                                                                                                           Isolated nucleic acid encoding a mutant hepatitis C virus (HCV) NS5B polymerase, useful for producing the mutant RNA polymerase which can used for identifying inhibitors that can treat HCV infection.
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                                                                                                                                 Gao
                                                                                                                                 Parge HE,
                                                                                                                               Hickey MJ,
                              07-MAY-2002; 2002EP-00009387.
                                                               10-MAY-2001; 2001US-0289829P
                                                                                                                                                                                                                                                                Claim 7; Page; 32pp; English
                                                                                                                               Diehl W,
                                                                                                (AGOU-) AGOURON PHARM INC
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The invention relates to an isolated, purified nucleic acid molecule, which encodes a mutant hepatitis C virus (HCV) NS5B RNA polymerase, where a point mutation occurs at least at one or all of positions 47, 101, 106, and/or 114 of the native RNA polymerase sequence not defined in the specification. The method of the invention is utilised to identify inhibitors of the polymerase. The inhibitors serving as lead compounds for the design of potentially therapeutic compounds for the treatment of HCV. The mutant HCV NS5B RNA polymerase has improved crystallisation properties as compared to a native HCV NS5B RNA polymerase. This sequence represents a mutant RNA polymerase protein of the invention. NOTE: This sequence is not shown in the specification. It is, however, described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA
                                                                                                241 QCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS
                                                                                                                                                           305 AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
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                                                                                                                                                                                                                                                                                             361 ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid encoding a mutant hepatitis C virus (HCV) NS5B polymerase, useful for producing the mutant RNA polymerase which can used for identifying inhibitors that can treat HCV infection.
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Matches 555; Conservative
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NSSB RNA h can be

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The present invention provides the hepatitis C virus (HCV) NSSB oblymerase protein and its structure. It also provides methods for identifying inhibitors of the protein which can be used in the treatment of HCV infection. HCV can lead to cirrhosis and hepatoma in its chronic
                                                                                     New polypeptide, derived from hepatitis C virus (HCV) polymerase NS5B, having a HCV polymerase activity, useful for crystal structure analysis and for rational identification of HCV polymerase inhibitors.
                                                                                                                                    Disclosure; Page 279-282; 295pp; English
                                           Miyano M, Adachi T;
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the specification and its sequence has been obtained from an electronic
data file
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                                                                96.4%; Score 2944; DB 6;
96.2%; Pred. No. 3.5e-274;
ive 13; Mismatches 9;
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                                           Sequence 576 AA;
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                                                                                       4 MSMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQV
                                                                                                                                                                               LDDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTL
                                                Gaps
                                              2,
Query Match 96.3%; Score 2942; DB 4; Length 579; Best Local Similarity 96.0%; Pred. No. 5.5e-274; Matches 556; Conservative 12; Mismatches 9; Indels
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WO2003014377-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAG79556-61 are hepatitis C virus (HCV) decreased affinity NS5B polymerases. These enzymes are used in the method of the invention for identifying a potential inhibitor of the binding between a HCV NS5B RNA-dependent RNA polymerase and an appropriate primer-template. The method comprises incubating the HCV NS5B polymerase with the primer-template. The template in the presence and absence of a potential inhibitor. The HCV NS5B polymerase has a decreased affinity for the primer-template relative to that of native HCV NS5B RNA-dependent RNA polymerase. The method is useful for identifying a potential inhibitor of the binding between a HCV NS5B RNA-dependent RNA polymerase and a primer-template. Use of polymerase constructs having a lower affinity towards the primer-template in that of native NS5B polymerase is particularly useful for identifying potential inhibitors in screening large libraries of compounds. The new method reduces the difficulties and disadvantages of prior art. The present method provides an assay that is easy to perform the control inhibitors that would not be identified as such using native NS5B polymerase. This protein represents a soluble form of mature HCV NS5B polymerase. This protein represents a soluble form of mature HCV NS5B polymerase. This protein represents a soluble form of mature HCV NS5B polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKWALYDVVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying inhibitors HCV NS5B RNA-dependent RNA polymerase, comprises incubating an HCV NS5B polymerase having decreased affinity for the primer template relative to the native polymerase, with a potential
                                       Enzyme, hepatitis C virus; HCV; decreased affinity; NS5B; polymerase;
inhibitor; RNA-dependent RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLROKKVTFDRLQVL
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             HCV decrease-affinity NS5B polymerase, NS5Bdelta21C-HT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.1%; Score 2936; DB 5;
95.5%; Pred. No. 2.1e-273;
ive 18; Mismatches 6;
                                                                                                                                                                                                                          (BOEH ) BOEHRINGER INGELHEIM CANADA LTD
                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 47-48; 52pp; English
                                                                                                                                                                                              08-MAR-2001; 2001US-0274374P.
                                                                                                                                                                  06-MAR-2002; 2002WO-CA000323
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Best Local Similarity 95.5
Matches 552; Conservative
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                                                                                                                                                                                                                                                                               WPI; 2002-698759/75.
                                                                                 Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 578 AA;
                                                                                                             WO200270739-A2
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                                                                                                                                       12-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                    nhibitor
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The invention relates to a method for identifying compounds that bind to hepatitis C virus (HCV) polymerase. The method involves (a) treating HCV polymerase, or its analogue, with a probe that binds to the polymerase to form a complex but is displaceable by an inhibitor; (b) measuring a signal emitted from the probe in the complex to establish a baseline value; (c) incubating the complex with test compound; and (d) measuring the signal from the complex and comparing it with the baseline. Any method is used to identify (also to determine potency) of HCV polymerase. The method is used to identify (also to determine potency) of HCV polymerase inhibitors, potentially useful as antiviral agents. The present sequence
241 QCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS 300
                                                                                                                                                                                                                                               424
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                                                                                                                                              AACRAAKLQDCTMLVNGDDLVV1CESAGTQEDAANLRVFTEAMTRYSAPPGDLPQPEXDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGKYLFNWAVRTKLKLTTPIP
                                                                                                                                                                                                                                               ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                      ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAMETARHTPINSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                   425 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP
                                                                                                           AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV; polymerase; virucide; hepatotropic; antiviral; enzyme; NS5B.
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96.1%; Score 2936; DB 6; Length 578;

Query Match

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                                                                           DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                               DDHYRDVLKEMKAKASTVKAKLLSVERACKLTPPHSAKSKFGYGAKDVRNLSSKAVDHIR 120
                                                                                                                                              SVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 180
                                                                                                                                                                                                                                                                                                      ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Thr, Val
/note= "Preferred amino acid at this position is valine.
Wild type residue at this position is threonine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crystallisation; crystal structure; hepatitis C virus; HCV; NSSB polymerase; NSSB RNA-dependent RNA polymerase; x-ray diffraction; atomic coordinate determination; drug screening; mutant; mutein; protein co-ordinate data; enzyme; His-NSSBdelCT21.
                                                                                                                                                                               TLPQAVMGSSYGFQXSPKQRVEFLVNAWKSKKCPMGFSYDTRCFDSTVTESDIRVEESIY
                                                                                                                                                                                                                                                           AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                                                                                                                                                                                                                      AACRAAKLQDCTMLVNGDDLVV1CESAGTQEDAANLRVFTEAMTRYSAPPGDLPQPEYDL
                                                                                                                                                                                                                                                                                                                   ELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAMETARHTPINSWLGNIIMYAPTLW
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                                                                                                                                                                                                                                                                                                                                                                                             EINRVASCIRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP
                                                    SMSYTWTGALITPCAAEESQLPINALSNSLVRHRNMVYSTTSRSAALRQKKVTFDRLQVL
                                                                                                                        SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                              QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA
                                SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
                                                                                                                                                                    TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wild type residue at this position is valine
          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AASRLDLSGWFVAGYSGGDIYHSLSRARPR--HHHHHH 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AASRLDLSGWFVAGYNGGDIYHSLSRARPRLEHHHHHH 578
2.1e-273;
ches 6;
95.5%; Pred. No. 2.10 ive 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG72214 standard; protein; 576
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Synthetic.
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          552; Conservative
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Misc-difference 335
Similarity
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The present invention relates to the purification, crystallisation, and structure of hepatitis C virus (HCV) NS5B RNA-dependent RNA polymerase. The composition containing the crystals of HCV NS5B polymerase polypeptide diffracts x-rays for determination of the atomic coordinates of the polypeptide to greater than 4.0 Angstroms resolution. The crystal is useful for determination of the atomic coordinates of the HCV NS5B polypeptide, and is useful in drug screening methods. The present sequence represents a mutant of the published sequence (Genbank Accession No. 130458) for the HCV NS5B polypeptide, His-NS5BdelCT21. This mutant terminus. The C-terminal 21 amino acid substitutions and a polyhistidine tag at the N-terminus. The C-terminal 21 amino acids present in the wild type are also deleted in His-NS5BdelCT21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New crystalline Hepatitis C Virus NS5B polypeptide composition useful for determining the atomic coordinates of the polypeptide and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDLAPEARQAIRSLTERLYVGGPMTNSKGONCGYRRCRASGVLTTSCGNTLTCYLKAAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 HYRDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 SYTWIGALITPCAAEESKLPINALSNSLLRHFINWYATTSRSAGLRQKKVTFDRLQVLDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 SYTWICALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLROKKVIFDRLQVLDD
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          this ;
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/note= "Preferred amino acid at
glutamine. Wild type residue at
arginine"
                                                                                                                                                                                                                                                                                                                                                                     Mannarino AF,
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les 545; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     Hong Z,
                                                                                                                                                                                                                                                                   03-APR-2000; 2000US-00541990
                                                                                                                                                                                                                 03-APR-2000; 2000US-00541990
                                                                                                                                                                                                                                                                                                                                                                     Cable M,
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Length 576; Indels 126 128 186 188 246 248 306 308 366 368 426 428 486 488

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NRVASCIRKLGYPPLRVWRHRARSVRAKLISQGGRAAICGKYLFNWAVRTKLKIJPIPAA 546
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                                                                                                                          9 SYTWIGALITPCAAEBSKIPINALSNSLLRHHNWYATISRSAGLRQKKVIFDRLQVLDD
                                                                                                                                                                                  67 HYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIRSV
                                                                                                                                                                                                         69 HYRDVLXEMKAKASTVXAXLLSVEBACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSV
                                                                                                                                                                                                                                                                                         129 WKDLLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTL
                                                                                                                                                                                                                                                                                                                                                                       189 PQVVMGSSYGEQYSPGQRVEFLVNTWKSKRNPMGFSYDTRCFDSTVTENDIRVEESIYQC
                                                                                                                                                                                                                                                                                                                                                                                                                                247 CDLAPEARQAIRSLITERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLICYLKAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 ITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLWAR
                                                                                                  7 SYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLRQKKVTFDRLQVLDD
                                                                                                                                                                                                                                                                  127 WKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTL
                                                                                                                                                                                                                                                                                                                                                  POAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIYQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV NS5B RNA-dependent RNA polymerase (RdRp) protein.
                     94.2%; Score 2879; DB 8; 96.0%; Pred. No. 6.5e-268; ive 11; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574
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                  Query Match
Best Local Similarity 96.0%
Matches 545; Conservative
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                                       HCV; RNA-dependent RNA polymerase; NS5B; cation exchange chromatography; polyethylene glycol; crystallisation; tNS5B; truncated NS5B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crystalline composition comprising a hepatitis C virus (HCV) RNA dependent RNA polymerase NS5b polypeptide, useful for providing a target for discovery of anti-HCV agents.
NRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKUTPIPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber PC;
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                                                                                                                          549 SXLDLSGWFVAGYSGGDIYHSLSRARPR 576
                                                                                                547 SRLDLSGWFVAGYSGGDIYHSLSRARPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                           ADH74494 standard; protein; 576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Thr, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= Val, Ala
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                                                                                                                                                                                                                                                                                                                           (first entry)
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(HONG/) HONG Z.
(MANN/) MANNARINO A F.
(WEBE/) WEBER P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cable M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          API; 2004-119171/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LESB/) LESBURG C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-HCV agent.
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                                                                                                                                                                                                                                                                                                                           25-MAR-2004
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                  487
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27-FEB-2001; 2001KR-00009873

(LGLI-) LG LIFE SCI LTD

Sequence 576 AA

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Enzyme; hepatitis C virus; HCV; decreased affinity; NS5B; polymerase;
inhibitor; RNA-dependent RNA polymerase.
HCV decrease-affinity NS5B polymerase, NS5Bdelta57-HT
                                                                                                                        06-MAR-2002; 2002WO-CA000323
                                                                                                                                              08-MAR-2001; 2001US-0274374P
                                                       Hepatitis C virus
                                                                             WO200270739-A2
                                                                                                  12-SEP-2002
                                                                                                                                                                                         Kukolj G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                      The invention relates to a novel recombinant Hepatitis C virus (HCV) NSSB protein which is derived from a HCV patient's serum and has excellent RNA dependent RNA polymerase (RdRp) activity. The polypeptide of the invention may be useful as a HCV growth inhibitor. The current sequence is that of the HCV NSSB RNA-dependent RNA polymerase (RdRp) protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544
                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                           SVWKDLIEDTETPINTTIMAKSEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCCDLAPEAROAIRSLTERLYVGGPMTNSKGONCGYRRCRASGVLTTSCGNTLTCYLKAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                                                                      64
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                                                                 Recombinant hepatitis C virus ns5b protein, and preparation process and
                                                                                                                                                                                                                                                                                                                                                                                                                 ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIQRLHGLSAFSLHSYSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP
                                                                                                                                                                                                                                                                                         SMSYSWIGALITPCAAEESKLPINPLSNSLLRHHNMVYATISRSAGLRQKEVIFDRLQVL
                                                                                                                                                                                                                                                                                                               DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
                                                                                                                                                                                                                                                                                                                                                           SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                                                                                                                                      TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                                                                                                     SMSYTWICALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLRQKKVIFDRLQVL
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                                                                                                                                                                                                                           Length 567;
                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                        y Match 93.2%; Score 2846; DB 7; Local Similarity 94.7%; Pred. No. 9.6e-265; hes 537; Conservative 17; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 AASRLDLSGWFVAGYSGGDIYHSLSRA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 AASRIDLSGWFVAGYSGGDIYRSLSRA 567
            Noh GY;
                                                                                                  Claim 3; SEQ ID NO 8; 19pp; Korean
            Lee MG,
                                 WPI; 2003-253755/25
            Hyun US, Kim JM,
                                            N-PSDB; ADM69006
                                                                                                                                                                                                     Sequence 567 AA;
                                                                                                                                                                                the invention.
                                                                           use thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSSB RNA-dependent RNA polymerase and a primer-template. Use of polymerase constructs having a lower affinity towards the primer-template than that of native NSSB polymerase is particularly useful for identifying potential inhibitors in screening large libraries of compounds. The new method reduces the difficulties and disadvantages of prior art. The present method provides an assay that is easy to perform on large libraries of compounds, and has improved sensitivity for detecting inhibitors that would not be identified as such using native NSSB polymerase. This protein represents a soluble form of mature HCV NSSB which lacks the C-terminal 57 amino acids and has an C-terminal hexa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
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                                                                                                                                                                                               comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    incubating an HCV NS5B polymerase having decreased affinity for the primer template relative to the native polymerase, with a potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.5%; Score 2734.5; DB 5; Length 545; 90.1%; Pred. No. 5.1e-254; ive 19; Mismatches 7; Indels 31;
                                                                                                                                                                                               Identifying inhibitors HCV NS5B RNA-dependent RNA
(BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 48-49; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.1
Matches 519, Conservative
                                                                  Mckercher G;
                                                                                                                             WPI; 2002-698759/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 545 AA;
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AAG79559 standard; protein; 545 AA

(first entry)

09-DEC-2002

AAG79559

AAG79559 ID AAG7 XX AC AAG7 XX DT 09-D XX

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                                                                                                                                                                             BINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIP 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - for
                                      241 QCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAS
                                                                                                                          ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG
                         AACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
                                                                          ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A nucleic acid fragment coding Non-A Non-B Hepatitis virus antigens diagnosis of NANBH and detection of HCV.
                                                                                                                                                                                          Non-A non-B hepatitis virus antigens; NANBH; hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 462;
                                                                                                                                                                                                                               545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRHHHHH 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.6%; Score 2279; DB 2; 93.0%; Pred. No. 3.2e-210; ive 18; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
(SANW) SANWA KAGAKU KENKYUSHO CO.
(IDDEU ) TONEN CORP.
(KOKU-) KOKUSAI SHIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus 8003-9388 fragment antigen.
                                                                                                                                                                                                                                                                                                                      AAR58592 standard; protein; 462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 16; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93JP-00193104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92JP-00207391
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-298800/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1994.
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Best Local S:
Matches 426,
                         305
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   236
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                                                                                                                                                                                 416
                                                                                                                                                                                                 241 PPRPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPSTPLARAAMETARHTPVNSWLGNI 300
                                                                                                                                                                                                                                           476
                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                       536
                                                                                                                                                                                                                                                                                                                         361 SLHSYSPGEINRVASCLRKIGVPPLRVWRHRARSVRAKILSQGGRAATCGKYLFNWAVRT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-A-non-B type hepatitis virus nucleic acid fragment useful for diagnosing non-A-non-B-hepatitis patient and non-A-non-B type hepatitis virus carrier.
 MALYDVVSTLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTEND
               61 MALYNVVSTLPQAVMGSSYGLQYSPGQRVBFLVNAWKSKKCPMGFSYDNRCFDSTVTESD
                                                                          301 IMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAF
                                                          IRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNT
                                                                                                                      LTCYLKAAAACRAAKLQDCTMLVNGDDLVV1CESAGTQEDAASLRVFTEAMTRYSAPPGD
                                                                                                                                                                                                                                          IMYAPTLWARMILMTHPFSILLLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAF
                                                                                                                                                                               PPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAMETARHTPVNSWLGNI
                                                                                                                                                                                                                                                                                                       SLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRT
                                                                                                                                                                                                                                                                                                                                                                  KLKLTPIPAASRLDLSGWFVAGYSGGDIYHSLSRARPR 574
                                                                                                                                                                                                                                                                                                                                                                                   non-A-non-B type hepatitis virus antigen;
hepatitis C virus antibody detection; clone C260-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus protein (clone C6-82).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL17783 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KOKU-) KOKUSAI SHIYAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-085213/09.
N-PSDB; ADL17778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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177
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Similarity

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SRAVNHIRSVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEK 176

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AAR29906 standard; protein; 389
  94JP-00032201
                    (EISA ) EISAI CO LTD
                                     Obara T,
                                                                    WPI; 1995-015655/03.
N-PSDB; AAQ75819.
                                                                                                                                                                                                                                                                    Sequence 547 AA;
   02-MAR-1994;
                                       Aoyama M,
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                                                 Arima T;
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 non-A-non-B type hepatitis virus protein fragment of the invention, NOTB: This sequence is given in the sequence listing as an embedded protien and is not further referred to in the specification.
                                                                                                SRAVNHIRSVWKDLLEDTDIPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEK 176
                                                                                                                                                61 MALYNVVSTLPQAVMGSSYGLQYSPGQRVEFLVNAWKSKKCPMGFSYDNRCFDSTVTESD 120
                                                                                                                                                                                     IMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAF 476
                                                                                                                                                                                                                                                                                                                                                  SLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGKYLFNWAVRT 420
                                                                                                           1 SKAVNHIRSVWKDLLEDNVTPVDTTVWAKSEVFCVQPEKGGRKPARLIVFPDLGVRVYEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-A Non-B hepatitis virus; structural region; cDNA to genomic RNA; detection; reagent; anti-Non-A Non-B hepatitis virus antibody; vaccine; antigen; epitope; diagnosis.
                                                                                                                                                                                                                                                                                                          MALYDVVSTLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTEND
                                                                                                                                                                            IRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNT
                                                                                                                                                                                                                   LTCYLKAAAACRAAKLODCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGD
                                                                                                                                                                                                                                                                                                                                      SLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRT
                                                                                                                                                                                                                                                        PPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNI
                                                                             Gaps
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/note= "putative epitope site (see AAR67641)"
                                                          Length 462
                                                        74.6%; Score 2279; DB 8; Length 4 93.0%; Pred. No. 3.2e-210; ive 18; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                          XLKLTPIPAASRLDLSGWFVAGYSGGDIYHSLSRARPR 574
                                                                                                                                                                                                                                                                                                                                                                                      Non-A Non-B hepatitis virus non-structural protein.
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non-A-non-B type hepatitis virus
This sequence is given in the seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                Local Similarity 93.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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non-B hepatitis virus.
                                      Sequence 462 AA;
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25-MAR-2003
18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1993;
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                                                                                                                                                   New non-A non-B hepatitis virus sub-type - used to develop prods. for detection, diagnosis, prevention and treatment of non-A non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FTTSMGNTWTCYIKALAACKAAGIKDPIMLVCGDDLVVISESQGNEEDERNLRAFTEAWT
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70.2%; Score 2144; DB 2;
Best Local Similarity 75.5%; Pred. No. 4.4e-197;
Matches 397; Conservative 55; Mismatches 74;
Sawada T,
                                                                                                                                                                                                                                 Claim 1; Page 33-37; 59pp; English.
Tohmatsu J,
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Clone, polypeptide, NS4-NS5; Hepatitis C; Virus; HCV; serum; HC; transcriptase; cDNA; primer; allele; core; region; upstream; hydrophilic; turn structure; alpha helix; beta sheet; antigen; determinant; antiserum.
                                                                                                                                                                                                                                                                                                                                                           New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                              'note= "Nonsense mutation"
                                                                                                                                                                /note= "Nonsense mutation"
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 257-59; 305pp; English
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Seki M, Honda Y, Takahashi K,
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91JP-00172794.
91JP-00287008.
91JP-00332329.
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                                   (first entry)
                                                     HCV NS4-NS5 peptide 030-4.
                           (revised)
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                                                                                                                                    Misc-difference 377
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                                                                                                          Hepatitis C virus
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                        25-MAR-2003
26-APR-1993
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12-JUL-1991;
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16-DEC-1991;
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        AAR29906;
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Teranishi Y, Hayashi N;

Murakami T,

The sequences given in AAR29871-906 and AAR29533 are encoded by various clones of the NS4-NS5 regions of the Hepatitis C virus (HCV) gene of the invention. These NS4-NS5 RNA sequencess were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32565-77. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different calleles of the same region of the HCV gene. Sequence analysis shows that these clones represent the core region and some upstream sequences of HCV. These polypeptides are thought to contain a highly hydrophilic region which can adopt a "turn structure" which is not an alpha helix or a beta sheet. These polypeptides are thought to act as antigen determinants and are highly reactive with antiserum raised against HCV-associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to

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                                                                     220 GFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCG 279
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59.3%; Score 1812; DB 2; Length 389; 96.1%; Pred. No. 2.6e-165; ive 6; Mismatches 8; Indels (
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61 YRRCRASGVLTTSCGNTLTCYLKASAACRAAKLQDCTMLVCGDDLVVICESAGTQEDAAS 120

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                121 LRVFTEAMTRYSAPPGDPPQDEYDLELITSCSSNVSVAHDASGKRVYYLTRDPPTPLARA
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C;Species: hepatitis C virus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0880
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C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: JQ0879
RjOkamcto, H.
submitted to JIPID, January 1991
A;Description: The 5'-terminal and 3'-terminal sequences of the A;Description: The 5'-terminal and 3'-terminal sequences of the A;Description: JQ0879
A;Accession: JQ0879
A;Accession: JQ0878
A;Residues: 1-365 < OKA>
A;Residues: 1-365 < OKA>
A;Cross-references: UNIPROT;Q81717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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Pred. No. 7e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: strain J4
C, Superfamily: hepatitis C virus genome polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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PQ0558
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A; Note: host Pan troglodytes (chimpanzee)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C; Accession: PS0104
R; Takeuchi; K.; Boonmar, S.; Kubo, Y.; Katayama, T.; Harada, H.; Ohbayashi, A.; Choo, Q.I
Gene 91, 287-291, 1990
A; Title: Hepatitis C viral cDNA clones isolated from a healthy carrier donor implicated in A; Reference number: PS0102; MUID:91007289; PMID:2170237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CjAccession: P80102
R;Takeuchi, K.; Boonmar, S.; Kubo, Y.; Katayama, T.; Harada, H.; Obbayashi, A.; Choo, Q.I
R;Takeuchi, Z87-291, 1990
A;Title: Hepatitis C viral cDNA clones isolated from a healthy carrier donor implicated i A;Reference number: P80102; MUID:91007289; PMID:2170237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 LAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEINRVASCLRKLG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome polyprotein - hepatitis C virus (isolate J1) (fragments)
N;Contains: NS5 protein; structural protein
C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 HDASGKRVYYLTRDPTVPLARAWETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 LIRDPTVPLARAMETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A,Residues: 1-259 <TAK>
A,Residues: 1-259 <TAK>
A,Cross-references: UNIPROT:081617; GB:D90077; GB:D90080
A,NOte: the authors translated the codon TGT for residue 255 as Lys
C,Superfamily: hepatitis C virus genome polyprotein
C,Keywords: polyprotein
F;1-117/Product: structural protein (fragment) #status predicted <SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: genomic RNA
A;Residues: 1-284 <TAK>
A;Cros-references: UNIPROT:(081633; GB:D90078; GB:D90079
A;Note: the authors translated the codon TGT for residue 274 as Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: hepatitis C virus genome polyprotein
K;Reywords: polyprotein
F;1-129/Product: structural protein (fragment) #status predicted ·
F;130-284/Product: NSS protein (fragment) #status predicted <NSS>
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                                                                                                                                                                                                                      genome polyprotein - hepatitis C virus (isolate pt) (fragments)
N;Contains: NS5 protein; structural protein
C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.3%; Score 774; DB 2; Length 28 Best Local Similarity 88.6%; Pred. No. 6.6e-52; Matches 140; Conservative 13; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 VPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVR 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 VPPLRAWRHRARSVRARLLARGGRAAICGKYLFNWAVR 284
                                                    181 TOEDAASLR 189
               333 TQEDAASLR 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: PS0104
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R;Okamoto, H. submitted to JIPID, January 1991
A;Description: The S'-terminal and 3'-terminal sequences of the genomic RNA of hepatitis A;Reference number: JQ0879
A;Accession: JQ0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translation not shown
A;Molecule type: genomic RNA
Ksesidues: 1-189 <XULD.
A;Cross-references: UNIPROT:Q68959; EMBL:X59934; NID:g556891; PIDN:CAA42557.1; PID:g4388
C;Superfamily: hepatitis C virus genome polyprotein
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C;Species: hepatitis C virus
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: $60587
R;Xu, L.Z.; Martinot-Peignoux, M.; Marcellin, P.; Benhamou, J.P.; Larzul, D.
J. Hepatol. 20, 598-602, 1994
A;Title: Comparison of the sensitivity of nested PCR in the 5' non-coding and the NSS A;Reference number: $60587; MUID:94351175; PMID:8071535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKGONCGYRRCRASGVLTTSCGNTLTCYLKASAACRAAKLODCTMLVCGDDLVVICESGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSCGNTLTCYIKAQAACRAAGLRDCTMLVCGDDLVVICESQGVQEDAASLRAFTRAMTRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERL 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLF 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAKKCPMGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTN 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKGONCGYRRCRASGVLTTSCGNTLTCYLKAAAACRAAKLQDCTMLVNGDDLVVICESAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVTENDIRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGONCGYRRCRASGVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSCGNTLTCYLKAAAACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPPGDPPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 54.2%; Score 1655; DB 2; Length 3 Local Similarity 88.7%; Pred. No. 1.7e-119; es 305; Conservative 22; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 NWAVRIKLKLTPIPAASRLDLSGWFVAGYSGGDIYHSLSRARPR 574
                                                                                                                                                                                                             A,Cross-references: UNIPROT:081716
A,Experimental source: strain J1
C,Superfamily: hepatitis C virus genome polyprotein
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                                                                                                                                                  A; Molecule type: genomic RNA
A; Residues: 1-365 < OKA>
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A; Cross-references: UNIPROT: 070640; GB: D10644; GB: D90553; NID: 9221666; PIDN: BAA01491.1; I
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66 RHRARSVRARLLARGGRAAICGKYLFNWAVRTKLKTFPIAAAGQLDLSGGWFTAGYSGGDI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 STVTENDIRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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C;Daces: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PG1277
R;Enomoto, N.; Tanaka, A.; Nakao, T.; Date, T.
Biocham. Biophys. Res. Commun. 170, 1021-1025, 1990
A;Fille: There are two major types of hepatitis C virus in Japan.
A;Reference number: PC1274; MUID:90358793; PMID:2117923
                                                                                                                                                                                                                                                                                    C;Spēcies: hepatītis C virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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R;Enomoto, N.; Tanaka, A.; Nakao, T.; Date, T.
Bjochem. Blophys. Res. Commun. 170, 1021-1025, 1990
A;Title: There are two major types of hepatitis C virus in Japan. A;Reference number: PC1274; MUID:90358793; PMID:2117923
A;Accession: PC1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.6%; Score 569; DB 2; Length 113; 95.6%; Pred. No. 1.1e-36; tive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                              NS5 protein - hepatitis C virus (strain K1-4) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NS5 protein - hepatitis C virus (strain K1-3) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 563; DB 2;
Pred. No. 3.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: NS5
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein
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C;Keywords: capsid protein
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94.7%;
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Best Local Similarity 95.6%;
Matches 108; Conservative
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126 YHSVSHARPR 135
                                                                                  565 YHSLSRARPR
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Best Local Similarity
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A; Residues: 1-113 <ENO>
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A; Residues: 1-113 < ENO>
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 17-Nov-2000
C;Gcession: D39109
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: D39109
A;Accession: preliminary
A;Residues: 1-156 <HAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q68962; EMBL:X78954; NID:g475176; PIDN:CAA55551.1; PID:g9398 (S.Superfamily: hepatitis C virus genome polyprotein C;Keywords: polyprotein F:1-135/Product: NS5a protein #status predicted <MAT>
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  118 LTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEKAL 177
                                                                               147 EVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTLPQAVMGSSYGFQYSPKQRVB 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 FLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIRSLTERLYV 266
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                                                                                                                                                                                                                                                                                                                                      genome polyprotein - hepatitis C virus (fragment)
N;Contains: NS5a protein
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: 13.Jan.-1995 #sequence_revision 26.Jul-1996 #text_change 09.Jul-2004
C;Accession: S44214
R;Feucht, H.H.
submitted to the EMBL Data Library, April 1994
A;Reference number: S44213
A;Reference number: S44214
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21.8%; Score 667; DB 2;
Best Local Similarity 91.9%; Pred. No. 4.1e-44;
Matches 124; Conservative 6; Mismatches 5.
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89.2%; Pred. No. 3:5e-41;
iive 8; Mismatches 6;
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                         508 ARSVRAKLLSQGGRAAICGKYL 529
                                                                                                                                                                                          238 ARSVRAKLLSQGGRAATCGKYL 259
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Matches 116; Conservative
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A; Residues: 1-135 < FEU>
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C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: capsid protein

A, Molecule type: mRNA A;Accession: PC1274

C;Genetics:

tch 18.4%; al Similarity 95.6%; 108; Conservative

Query Match Local

Best Loca Matches

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A; Accession: PCL279
A; Molecule type: mRNA
A; Residues: 1-113 < ENO>
A; Residues: 1-113 < ENO>
A; Cross-references: UNIPROT:Q01193; GB:D10646; GB:D90555; NID:g221670; PIDN:BAA01493.1; I
                         A;Molecule type: mRNA
A;Residues: 1-113 <ENO>
A;Cross-references: UNIPROT:Q01185; GB:D10643; GB:D90552; NID:g221664; PIDN:BAA01490.1; I
C;Genetics:
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1282
R;Enomoto, N.; Tanaka, A.; Nakao, T.; Date, T.
Biochem. Biophys. Res. Commun. 170, 1021-1025, 1990
A;Title: There are two major types of hepatitis C virus in Japan.
A;Reference number: PC1274; MUID:90358793; PMID:2117923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: hepatitis C virus
C.bate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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R, Enomoto, N.; Tanaka, A.; Nakao, T.; Date, T.
Bicchem. Biophys. Res. Commun. 170, 1021-1025, 1990
A;Title: There are two major types of hepatitis C virus in Japan.
A, Reference number: PC1274; MUID: 90358793; PMID: 2117923
                                                                                                                                                                                                                                                                          Query Match 18.3%; Score 560; DB 2; Length 113; Best Local Similarity 93.8%; Pred. No. 5.4e-36; Matches 106; Conservative 5; Mismatches 2; Indels
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16.8%; Score 513; DB 2; L.
Best Local Similarity 85.7%; Pred. No. 2.2e-32;
Matches 96; Conservative 9; Mismatches 7;
                                                                                                                                                        A;Gene: NS5
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein
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A; Residues: 1-113 <ENO>
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A; Accession: PC1276
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A;Residues: 1-113 <ENO>
A;Cross-references: UNIPROT:Q01184; GB:D10642; GB:D90551; NID:g221662; PIDN:BAA01489.1;
                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-113 <ENO>
A;Cross-references: UNIPROT:Q01192; GB:D10641; GB:D90550; NID:g221658; PIDN:BAA01488.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSS protein - hepatitis C virus (strain K1-1) (fragment)
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Accession: PC1275
R;Enomoto, N.; Tanaka, A.; Nakao, T.; Date, T.
Biochem. Biophys. Res. Commun. 170, 1021-1025, 1990
A;Title: There are two major types of hepatitis C virus in Japan.
A;Reference number: PC1275.
A;Accession: PC1275.
                                                          C,Species: hepatitis C virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTSCGNTLFCYLKAAAACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRV 342
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                                                                                                                 C, Accession: FC1274
R; Enomoto, N.; Tanaka, A.; Nakao, T.; Date, T.
Biochem. Biophys. Res. Commun. 170, 1021-1025, 1990
A;Title: There are two major types of hepatitis C virus in Japan. A;Reference number: PC1274; MUID:90358793; PMID:2117923
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                             - hepatitis C virus (strain K1) (fragment)
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Pred. No. 3.8e-36;
2; Mismatches 3;
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C;Species: hepatitis C virus
C;Date: 30-5ep-1993 #sequence_revision 30-5ep-1993 #text_change 09-Jul-2004
C;Dates solves to the solves of the s NS5 protein - hepatitis C virus (strain K1-2) (fragment)

C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: capsid protein

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                                                                                                    1 STVTERDIRTEESIYQACSLPQEARTAIHSLTERLYVGGPMTNSKGQSCGYRRCRASGVF 60
                                       0; Gaps
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Delyprotein - hepatitis C virus (isolate T-9) (fragment)
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Joace: 30-Uon-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: PQ0275
R;Mori, S.; Kato, N.; Yagyu, A.; Tanaka, T.; Ikeda, Y.; Petchclai, B.; Chiewsilp, P.; Ku R;Mori, S.; Kato, N.; Yagyu, A.; Tanaka, T.; Ikeda, Y.; Petchclai, B.; Chiewsilp, P.; Ku R;Mori, B.; Apperence number: PQ0273; MulD:92181465; PMID:1311926
A;Accession: PQ0275

A;Cross-references: UNIPROT:Q81819; DDBJ:D10080; NID:g221684; PIDN:BAA00974.1; PID:g2216 A;Note: this sequence corresponds to NS5 protein C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: polyprotein A; Molecule type: genomic RNA A; Residues: 1-113 <MOR>

230 STVTENDIRVEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVL 289 1 STVTEHDIRTEEEIYQCCDLEPEARKAISALTERLYIGGPMYNSKGLQCGYRRCRASGVL 60 0; Gaps 13.9%; Score 426; DB 2; Length 11: 73.2%; Pred. No. 1.1e-25; tive 11; Mismatches 19; Indels Query Match Best Local Similarity 73.24 Matches 82, Conservative

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Length 113;

61 PTSFGNTITCYIKATAASRAAGLKDPSFLVCGDDLVVVSESCGVEEDRAALR 112 290 ITSCGNTLICYLKAAAACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLR 341 ઠે 셤

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Q66n9 hepatitis c Q66n1 hepatitis c Q66n2 hepatitis c Q66n2 hepatitis c Q66n2 hepatitis c Q66n7 hepatitis c Q66n7 hepatitis c Q66n7 hepatitis c Q66n7 hepatitis c Q66n9 hepatitis c Q66n9 hepatitis c Q66n9 hepatitis c

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DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
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Hepatitis C virus.
Viruses, seRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
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P SEQUENCE FROM N.A.

A Rather M., Lamson D., Wroblewski D., Reilly A., Philpott S.,

A Klainer D., Holman S., Augenbraun M., Taylor J.;

A Klainer D., Holman S., Augenbraun M., Taylor J.;

T "Sequence Analysis of Hepatitis C Virus Replication Functions in HCV/HIV Coinfected Subjects.";

I Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005524; F:RNA binding; IEA.

R GO; GO:0003722; F:RNA binding; IEA.

R GO; GO:0003722; F:RNA binding; IEA.

R GO; GO:0003725; F:RNA binding; IEA.

R GO; GO:00063725; F:RNA binding; IEA.
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Best Local Similarity 95.8%; Pred. No. 6.9e-218;
Matches 543; Conservative 13; Mismatches 11;
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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                                                                                                         305 AACRAAKLODCTWLVCGDDLVVICESAGTQEDEASLRVFTEAMTRYSAPPGDPPKPEYDL 364
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571 AA; 63249 MW; F76482BE94526FDA CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
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NCBI_TaxID=11103;
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245 QCCDLAPEARQAIRSLTERLYIGGPLINSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAT 304
                                                                                                                                               ELITSCSSNVSVAHDASGKRVXYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW 424
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066NA8;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
Kleiner D., Holman S., Augenbraun M., Taylor J.;

"Sequence Analysis of Hepatitis C Virus Replication Functions in
"Sequence Analysis of Hepatitis C Virus Replication Functions in
"HCV/HIV Coinfected Subjects";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AY682764, AAU08311.1;
InterPro; IPR001265; HCV_RdRP.
InterPro; IPR007095; RNA_POI_DS_PS.
InterPro; IPR007095; RNA_POI_DS_PS.
InterPro; IPR007094; RNA_POI_PSVir.

PF00999; Viral_RdRP; 1.
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571 AA, 63201 MW, 5590C9F59B69B2A0 CRC64;
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NCBI_TaxID=11103;
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Hepacivirus.
NCBI_TaxID=11103;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
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245 QCCDLAPEARQAIRSLIERLYIGGPLTNSRGQNCGYRRCRASGVLTTSCGNTLTCYLKAT 304
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Hepacivirus.
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Kleiner D., Holman S., Augenbraun M., Taylor J.;
Sequence Analysis of Hepatitis C Virus Replication Functions in HCV/HIV Coinfected Subjects ";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX682756; AX008313.1; -.
InterPro; IPR007036; HCV/RAPP.
InterPro; IPR007095; RNA_pol_PSV:
InterPro; IPR007095; RNA_pol_PSVir.
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25-CCT-2004 (TrEMBLrel. 28, La
25-CCT-2004 (TrEMBLrel. 28, La
Polyprotein (Fragment).
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      125 SVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
Hepacivirus.
NCRI_TAXID=11103;
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Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
Kleiner D., Holman S., Augenbraun M., Taylor J.;
Kleiner D., Holman S., Augenbraun M., Taylor J.;
Sequence Analysis of Hepatitis C Virus Replication Functions in
"Sequence Analysis of Hepatitis C Virus Replication Functions in
HCV/HIV Coinfected Subjects.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY682784; AAU03440.1; -.
InterPro; IPR007095; RNA_POL_DS_PS.
InterPro; IPR007095; RNA_POL_DS_PS.
InterPro; IPR007094; RNA_POL_PSvir.
Pfam; PF00998; Viral_RARP; 1.
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571 571
571 AA; 63317 MW; 4BC8ACIE98153857 CRC64;
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                                                                                           QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
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5 SMSYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTISRSASLRQKKVTFDRLQVL
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
NS5b (Fragment).
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
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Kleiner D., Holman S., Augenbraun M., Taylor J.;

"Sequence Analysis of Hepatitis C Virus Replication Functions in
"Sequence Analysis of Hepatitis C Virus Replication Functions in
HCV/HLV Coinfected Subjects."

I Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000523; F:RNA binding; IEA.

GO; GO:0005359; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0005359; P:tranacription; IEA.

R GO; GO:0019079; P:viral genome replication; IEA.

R InterPro; IPR001095; RNA_DOI DS PS.

InterPro; IPR007095; RNA_DOI DS PS.
InterPro; IPR007094; RNA_DOI DS PS.
InterPro; IPR007094; RNA_DOI PSVIr.

R PF00998; Viral_RGRP; I.
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95.2%; Pred. No. 2.6e-216;
tive 15; Mismatches 12; Indels
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571 AA; 63123 MW; 931743E7C7819F36 CRC64;
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Matches 540; Conservative
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65 DDHYRDVLKEMKAKASTVKAKLLSIEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVKHIR 124
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066NA2,
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TremBlrel. 28, Last annotation update)
Polyprotein (Fragment)
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
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Barker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
Kleiner D., Holman S., Augenbraun M., Taylor J.;
Kleiner D., Holman S., Augenbraun M., Taylor J.;
"Sequence Analysis of Hepatitis C Virus Replication Functions is
HCV/HIV Coinfected Subjects ";
Submitted (JUL_2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AK682760; AM06317.1; -.
InterPro; IPR002166; HCV RdRP.
InterPro; IPR007099; RNA_Pol_DS_PS.
InterPro; IPR007099; RNA_pol_DS_PS.
InterPro; IPR007099; RNA_pol_DS_PS.
InterPro; IPR007099; RNA_pol_DS_PS.
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92.9%; Score 2839; DB 2; Length 5
Best Local Similarity 94.5%; Pred. No. 3.3e-215;
Matches 536; Conservative 19; Mismatches 12; Indels
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571 AA; 63227 MW; FS4BDES50ACDEEBC CRC64;
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                                                125 SVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRRPARLIVFPDLGVRVCEKWALYDVVS 184
                                                                                                                                      TLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIY 244
                                                                                                                                                                       245 QCCDLAPEARQAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAT 304
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Hepacivirus.
NCBI_TaxID=11103;
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Kleiner D., Holman S., Augenbraun M., Taylor J.;
"Sequence Analysis of Hepatitis C Virus Replication Functions in Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY682780; AAU08336.1;
InterPro; IPR002166; HCV_RdRP.
InterPro; IPR007095; RNA_POL_DS_PS.
InterPro; IPR007095; RNA_POL_DS_PS.
InterPro; IPR007094; NNA_POL_PSVIr.
Pfam; PF009998; Viral_RdRP; 1.
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93.2%; Score 2846; DB 2; Length 571;
Best Local Similarity 94.9%; Pred. No. 9.3e-216;
Matches 538; Conservative 17; Mismatches 12; Indels (
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25-OCT-2004 (TrEWBLrel. 28, Created)
25-OCT-2004 (TrEWBLrel. 28, Last sequence update)
25-OCT-2004 (TrEWBLrel. 28, Last annotation update)
Polyprotein (Fragment).
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NCBI_TaxID=11103;
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                                                                              185 TLPQAVMGSSYGFQXSPGQRVEFLVNAWKSKKNPMGFSYDTRCFDSTVTESDIRVEESIY
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBL_TaxID=11103;
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Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S., Rleiner D., Holman S., Augenbraun M., Taylor J.;

Rleiner D., Holman S., Augenbraun M., Taylor J.;

Sequence Analysis of Hepatitis C Virus Replication Functions : HCV/HIV Coinfected Subjects.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AY682785; AA00341.1; -

InterPro; IPR007045; RNA_Poll_DS_PS.

InterPro; IPR007095; RNA_Poll_DS_PS.

InterPro; IPR007099; RNA_Poll_DS_PS.

FRAM, PF009998; Viral_RGRF; 1.
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Matches 537; Conservative
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
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InterPro; IPR007095; RV RQRP.
InterPro; IPR007095; RNA_pol_DS PS.
InterPro; IPR007099; RNA_pol_PSvir.
Pfam; PP00998; Viral_RGRP; 1.
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571 AA; 63254 MW; 475D83341A64631B CRC64;
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5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNWVYATTSRSASQRQKKVTFDRLQVL
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Hepatitis C virus.
Hepatitis Ext. positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TAXID=11103;
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Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
Rleiner D., Holman S., Augenbraun M., Taylor J.;
Requence Analysis of Hepatitis C Virus Replication Functions
HCV/HIV Coinfected Subjects ";
Submitted (JUL_2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY682774, AM08330.1; -.
InterPro; IPR002166; HCV_RGRP.
InterPro; IPR007095; RNA_Pol_DS_PS.
InterPro; IPR007099; RNA_pol_DS_PS.
InterPro; IPR007099; RNA_pol_DS_PS.
InterPro; PR00999; Viral_RGRP; 1.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TAXID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S., Rainer D., Holman S., Augenbraun M., Taylor J.; Kleiner D., Holman S., Augenbraun M., Taylor J.; Sequence Analysis of Hepatitis C Virus Replication Functions is United (JUL_2004) to the EMBL/GenBank/DDBJ databases. EMBL, AY682789; AA00345.1; -.. InterPro; IPR002166; HCV_RGRP: InterPro; IPR007095; RNA_FOl_DS_PS.
InterPro; IPR007095; RNA_FOl_DS_PS.
InterPro; PR007099; Viral_RAPP; 1.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
Kleiner D., Holman S., Augenbraun M., Taylor J.;
Kleiner D., Holman S., Augenbraun M., Taylor J.;
"Sequence Analysis of Hepatitis C Virus Replication Functions in HCV/HIV Coinfected Subjects.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY682782; AAUG8309.1;
InterPro; IPR0071095; RNA_DOL_DS_PS.
InterPro; IPR007095; RNA_DOL_DS_PS.
InterPro; IPR0070998; Viral_RARP; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBL_TaxID=11103;
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Rleiner D., Holman S., Augenbraun M., Taylor J.;
Sequence Analysis of Hepatitis C Virus Replication Functions HCV/HIV Coinfected Subjects.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY682755; AA008312.1; -.
InterPro; IPR002166; HCW_RGRP.
InterPro; IPR007095; RNA_Pol_DS_PS.
InterPro; IPR007099; NNA_Pol_DS_PS.
InterPro; PR007099; NNA_Pol_DS_PS.
Fram: PF009998; Viral_RGRP; 1.
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571 AA; 62829 MW; 1EB09F6368B4B729 CRC64;
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1 MASWSMSYTWTGALITPCAA.....GGDIYHSLSRARPRHHHHH
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                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
      5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                        US-09-541-990A-1
US-08-867-611-10
US-08-867-611-10
US-09-03-591-10
US-07-681-103B-6
US-07-681-103B-6
US-08-487-103B-6
US-08-487-103B-6
US-08-485-500-6
PCT-US91-02370-6
PCT-US94-04174-6
US-08-184-236-2
US-07-681-703B-2
US-07-681-703B-2
US-08-487-410B-2
US-08-487-410B-2
US-08-487-410B-2
US-08-447-410B-2
US-08-447-410B-2
US-08-447-410B-2
US-08-447-410B-2
US-08-447-410B-2
US-08-447-410B-2
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US-08-447-41B-62
US-08-447-41B-62
US-08-647-611-12
US-08-67-611-12
US-08-67-611-12
US-08-67-611-12
US-08-67-611-12
US-08-67-611-12
US-08-67-611-12
US-08-644-418-60
                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-867-611-14
US-09-690-359-14
                                                                                                                                            513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                  SUMMARIES
       GenCore version (c) 1993 - 2005
                                                      September 22, 2005, 14:48:15
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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                                                                                    US-10-712-479-4
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               Copyright
                                                                                                                                                                           seq length: 0
seq length: 585
                                                                                                                    BLOSUM62
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Match
                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                    Scoring table:
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                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                      Sequence:
                                                                                                                                            Searched:
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                                                      Run on:
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128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leaburg, Charles A.
APPLICANT: Leaburg, Anchael
APPLICANT: Cable, Michael
APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
APPLICANT: Weber, Patricia
TITLE OF INVENTION: Compositions of Hepatitis C Virus NS5B Polymerase and
TITLE OF INVENTION: Methods for Crystallizing Same
FILE REFERENCE: IN098B US
CURRENT APPLICATION NUMBER: US/09/541,990A
CURRENT FILING DATE: 2000-04-03
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 HYRDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIRSV 126
    68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQVVMGSSYGFQYSPGQRVEFLVNTWKSKKRPMGFSYDTRCFDSTVTENDIRVEESIYQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYTWIGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 WKDLLEDTDTFIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                  Sequence 82,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: amino acids at 335, 344 and 550 may be threonine INFORMATION: or valine at 335, valine or alanine at 344 and INFORMATION: arginine or glutamine at 550
                                                                                                        Sequence
Sequence
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                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
                       Sequence
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PCT-US92-06965A-19
US-08-638-911A-41
US-08-638-911A-41
US-09-038-369B-82
US-09-399-048-82
US-09-899-048-82
US-09-899-048-58
US-08-81A-214
US-08-836-075A-54
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US-08-836-075A-64
US-08-846-075A-64
US-08-846-075A-64
US-08-846-075A-64
US-08-846-075A-64
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US-08-424-550B-396
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Patent No. 6434489
GENERAL INFORMATION:
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64 LDDHYRDVLKEMKAKASTVKAKTLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 NSVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 STLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEWART, JAMES L
RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPTRY: USA
ZIP: 60064-350

ZIP: 60064-350

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                               36.8%; Score 1124; DB 3;
84.8%; Pred. No. 2.4e-106;
tive 14; Mismatches 24;
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SEQ 10 NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DEVARE, SUSHIL G
DESAI, SURESH M
CASEY, JAMES M
DAILEY, STEPHEN H
DAWSON, GEORGE J
GUTIERREZ, ROBIN A
LESNIEWSKI, RICHARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09690359
Patent No. 6593083
GENERAL INFORMATION:
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  21-AUG-1991
                                                                                                                                                                                                                                                                                    LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 84.8
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 AAACRAAKLO 313
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                                                                                                             CRAAKLQDCTMLVNGDDLVVICESAGXQEDAASLRXFTEAMTRYSAPPGDPPQPEYDLEL 368
                                                                                                                                                                                                  369 ITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLWAR 428
                                                                                                                                                                                                                                                                                    MILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEI 488
                                                                                                                                                       ITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLWAR
                                                                                                                                                                                                                                            MILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEI
                                                                                                                                                                                                                                                                                                                               NRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLTPIPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DESAI, SURHIL G
APPLICANT: DESAI, SURESH M
APPLICANT: CASEY, JAMES M
APPLICANT: DAILBY, STEPHEN H
APPLICANT: DAILBY, SEPHEN H
APPLICANT: GUITERREZ, ROBIN A
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIC
STREET: ONE APPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,611
FILING DATE: 0.2-UN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,757
                                                                                                                                                                                                                                                                                                                                                                                                                                              549 SXLDLSGWFVAGYSGGDIYHSLSRARPR 576
                                                                                                                                                                                                                                                                                                                                                                                                                    SRLDLSGWFVAGYSGGDIYHSLSRARPR 574
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APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
PRICE APPLICATION DATE:
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/179,896
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                       489
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426

Gaps

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307 NSVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVV 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 TKLPLAVMGSSYGFQYSPGQRVBFLVQAWKSKKTPMGFSYDTRCFDSTVTESDIRTEEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 RSVWKDLLEDTDTPIQTTIMAKNEVPCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LDDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHI
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                                                                                               ZIP: 60065-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US92/06965A
FILING DATE: 19920821
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reyes, Gregory
APPLICANT: Reyes, Gregory
APPLICANT: Kim, Jungsuh P.
APPLICANT: Moeckli, Randolph
TITLE OF INVENTION: Hepatitis C Virus Epitopes
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peter J. Dehlinger
STREET: P.O. BOX 60850
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.8%; Score 1124; DB 5; 84.8%; Pred. No. 2.4e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
36.8%; Score 1124; D
Best Local Similarity 84.8%; Pred. No. 2.4e
Matches 212; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: POREMESKI, FRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834PC.02
RELECOMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEPHONE: 708-937-9566
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-853-985A-6
; Sequence 6, Application US/07853985A
; Patent No. 5436318
T: ONE ABBOTT PARK ROAD ABBOTT PARK
: ILLINOIS
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein PCT-US92-06965A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AAACRAAKLQ 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 STLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 RSVWKDLLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKA 303
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GENERAL INFORMATION:
APPLICANT: DEVARE, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
TITLE OF INVENTION: HCV SYNTHETIC PEPTIDE FROM NS1 REGION NORRESPONDENCE ADDRESS:
ADDRESSEE: ABBORT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.8%; Score 1124; DB 4; Length 4 Best Local Similarity 84.8%; Pred. No. 2.4e-106; Matches 212; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                FILING DATE: «Unknown»

APPLICATION NUMBER: US 07/572,822

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: US 07/748,561

FILING DATE: 07-NOV-1990

APPLICATION NUMBER: US 07/748,561

FILING DATE: 21-AUG-1991

APPLICATION NUMBER: US 07/748,565

FILING DATE: 21-AUG-1991

APPLICATION NUMBER: US 07/748,565

FILING DATE: 21-AUG-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: POREMBSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
                                                                                                  A APPLICATION DATA:
APPLICATION NUMBER: 08/867,611
BILING DATE: 02-JUN-1997
APPLICATION NUMBER: US/08/646,757
FILING DATE: «UNKNOWI»
APPLICATION NUMBER: US/08/179,896
                            APPLICATION NUMBER: US/09/690,359
FILING DATE: 17-Oct-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-690-359-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 708-937-9556
     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 AAACRAAKLQ 313
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487 RAACRAAGLQ 496
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426

Gaps

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LENGTH: 504 amino acids TYPE: amino acid
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 SVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVWKDILLEDIDIPIQTIIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.7%; Score 908; DB 1; Length 504; Best Local Similarity 87.2%; Pred. No. 3.9e-84; Matches 177; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reyes, Gregory
APPLICANT: Kim, Jungsuh P.
APPLICANT: Kim, Jungsuh P.
APPLICANT: Moeckli, Randolph
TILLE OF INVENTION: Hepatitis C Virus Epitopes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AURENY APPLICATION DATA:
APPLICATION NUMBER: US/07/681,703B
FILING DATE: 05-APR-1991
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,985A
FILING DATE: 19920320
CLIASSIFICATION DATA:
APPLICATION NUMBER: US 07/505,611
FILING DATE: 06-APR-1990
APPLICATION NUMBER: US 07/594,854
FILING DATE: 09-OCT-1990
ATMOREY/AGENT INCRMATION:
NAME: Deblinger, Peter J.
REGISTRATION NUMBER: 28,006
REGISTRATION NUMBER: 28,006
REGISTRATION NUMBER: 28,006
REGISTRATION NUMBER: 28,006
REGISTRATION NUMBER: 34,006
REGISTRATION INFORMATION:
TELEBENORE: 415-324-0880
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 504 amino acida TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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302 SMSYSWTGALVTPCAAEEQKLPINALSNSLLRHHNLVYSTTSRSACQRQKKVYFDRLQVL 361
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Pred. No. 3.9e-84;
7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08184236;
Patent No. 5538865;
GENERAL INFORMATION:
APPLICANT: Reyes Gregory
APPLICANT: Reyes Gregory
TITLE OF INVENTION: Hepatitis C Virus Epitopes
VINDER OF SEQUENCES: 10
CORRESONDENCES: 10
CORRESONDENCES: ADDRESSE: ADDRESSE: Deblinger & Associates
STREET: P.O. BOX 60850
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,611
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 594,854
FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-076.21
TELEPHONE (415) 324-0880
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUDIESS:

JUDIESS:

STREET: P.O. BOX 60850
CITY: Palo Alto
STATE: CA
COUNTRY: U°
ZIP:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,236
FILING DATE:
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PLING DATE: 06-APR-1990
APPLICATION NUMBER: US 07/594,854
FILING DATE: 09-OCT-1990
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MG-
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Best Local Similarity 87.2%;
Matches 177; Conservative
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REGISTRATION NUMBER: 33,875
                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICATION NUMBER:
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                                                                                                                                                                                                         US-08-407-410B-6
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; Sequence 6, Application US/08407410B
; Patent No. 5843636
; GENERAL INFORMATION:
    APPLICANT: Reyes, Gregory
; APPLICANT: Kim, Jungsuh P.;
    APPLICANT: Kim, Jungsuh P.;
    APPLICANT: Simonsen, Christian C.;
    TITLE OF INVENTION: Hepatitis C Virus Epitopes
    NUMBER OF SEQUENCES: 26
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Peter J. Dehlinger
    STREET: 350 Cambridge Ave., Suite 100
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,410B
APPLICATION NUMBER: US 07/853,985
FILING DATE: 20-MAR-1992
ATTORNEY/AGENT INPORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/POCKET NUMBER: 4600-0113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEPHONE: 415-324-0860
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
TOPOLOGY: linear
WOLECULE TYPE: protein
US-08-184-236-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 TLPQAVMGSSYGFQYSPKQRVEF 207
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,611
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 594,854
FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.2°
Matches 177; Conservative
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MEDIUM TYPE: Floppy
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362 DSHYQDVLKEVKAAAASKVKANLLSVEEACSLIPPHSAKSKFGYGAKDVRCHARKAVTHIN 421
                                                                                                                                                                                                                                                                                                                                                                                                          302 SMSYSWTGALVTPCAAEEQKLPINALSNSLERHHNLVYSTTSRSACQRQKKVTFDRLQVL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 SVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDDVT 481
                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                             Score 908; DB 2; Length 504;
Pred. No. 3.9e-84;
7; Mismatches 19; Indels
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COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reyes, Gregory
APPLICANT: Reyes, Gregory
APPLICANT: Rim, Jungsuh P.
APPLICANT: Moeckli, Randolph
APPLICANT: Simonsen, Christian C.
TITLE OF INVENTION: Hepatitis C Virus Epitopes
INVERS OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Peter J. Dehlinger
STREET: 350 Cambridge Ave., Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 594,854
FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REFERRICE/DOCKET NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 4600-076.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 323-8302
INFORMATION FOR SEQ ID NO: 6:
SEQUIENCE CHARACTERISTICS:
LENGTH: 504 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/407,410
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Patent No. 5843639
                                                                                                                                                                                                                                                                             29.7%;
                                                                                                                          : 504 amino acids
amino acid
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Best Local Similarity 87.2<sup>3</sup>
Matches 177; Conservative
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; MOLECULE TYPE: protein PCT-US91-02370-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 SVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVT 481
                                                                                                                                                                                                                                                                5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL 64
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                 29.7%; Score 908; DB 2; Length 504; larity 87.2%; Pred. No. 3.9e-84; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02370
FILING DATE: 19910405
CLASSIFICATION: 435.5
PRIOR APPLICATION NUMBER: US 505,611
APPLICATION NUMBER: US 505,611
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: US 594,854
FILING DATE: 09-OCT-1990
ATPOREY/AGENT INFORMATION:
ANALY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reyes, Gregory
APPLICANT: Reyes, Gregory
APPLICANT: Kim, Jungsuh P.
APPLICANT: Moeckli, Randolph
APPLICANT: Simonsen, Christian C.
TITLE OF INVENTION: Hepatitis C Virus Epitopes
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peter J. Dehlinger
STREET: P.O. BOX 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 4600-076.41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 TLPQAVMGSSYGFQYSPKQRVEF 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 KLPLAVMGSSYGFQYSPGQRVEF 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-500-6
  (415) 323-8302
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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  TELEPHONE:
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Best Local
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302 SMSYSWTGALVTPCAAEEQKLPINALSNSLIRHHNLVYSTTSRSACQRQKKVTFDRLQVL 361
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                                                                                                                                                                                                                      65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
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                                                                                                               5 SMSYTWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVL
                                                          Gaps
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Sequence 6, Application PC/TUS9404174
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory
APPLICANT: Kim, Jungeuh P.
APPLICANT: Kim, Jungeuh P.
APPLICANT: Mockil, Randolph
TITLE OF INVENTION: HCV Immunodiagnostic Antigens and Antibodies
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRES: 28
CORRESPONDENCE ADDRES: ADDRESSE: Law Offices of Peter J. Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
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     Length 504;
                                                       Indels
Score 908; DB 5;
Pred. No. 3.9e-84;
7; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600-0107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0860
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04174
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 XLPLAVMGSSYGFQYSPGQRVEF 504
                                                                                                                                                                                                                                                                                                                                                                                                                                       185 TLPOAVMGSSYGFOYSPKORVEF 207
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APPLICATION NUMBER: US 505,611
FILING DATE: 06-APP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
Query Match 29.7%;
Best Local Similarity 87.2%;
Matches 177; Conservative
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amino acid
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326 VICESAGTQEDAASLRVFTEAMTRYSAPPGDPQPEYDLELITSCSSNVSVAHDASGKRV 385
                               326 VICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDASGKRV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 VGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAAAACRAAKLQDCTMLVNGDDLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPFURER: BATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/681,7038
FTLING DATE: 05-APR-1991
                                                                                                                                                                                                                           Sequence 2, Application US/07681703B
Patent No. 5443965
GENERAL INPORMATION:
APPLICANT: Reyes, Gregory
APPLICANT: Moeckli, Randolph
TITLE OF INVENTION: Hepatitis C Virus Epitopes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 405-AFK-1291
CLASSIFICATION: 405-AFK-1291
CLASSIFICATION: 405-AFK-1291
APPLICATION DATA:
APPLICATION NUMBER: US 505,611
FILING DATE: 06-AFK-1990
APPLICATION NUMBER: US 594,854
FILING DATE: 09-ACT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 324-0880 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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amino acid
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                                          DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                  125 SVWKDILEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVS 184
                                                                                                                                                      422 SVWKDLLEDNVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVT 481
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                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07853985A
Patent No. 5436318
GENERAL INFORMATION:
APPLICANT: Rim, Jungsuh P.
APPLICANT: Moeckli, Randolph
TITLE OF INVENTION: Hepatitis C Virus Epitopes
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peter J. Dehlinger
STREET: P. O. BOX 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 4600-0076.22
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,985A
PILING DATE: 19920320
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,611
PILING DATE: 06-APR-1990
APPLICATION NUMBER: US 07/594,854
PILING DATE: 09-CCT-1990
APPLICATION NUMBER: US 07/594,854
PILING DATE: 09-CCT-1990
                                                                                                                                                                                                              185 TLPQAVMGSSYGFQYSPKQRVEF 207
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Best Local Similarity 87.6
Matches 163; Conservative
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STATE: CA
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US-08-407-410B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 EFLUNTWKAKKCPMGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIRSLTERLY
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                                                                                    Sequence 2, Application US/08184236;
Patent No. 5538865
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory
APPLICANT: Rowerli, Randolph
TITLE OF INVENTION: Hepatitis C Virus Epitopes;
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. BOX 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,236
FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: US 07/505,611
FILING DATE: 06-APR-1990
APPLICATION NUMBER: US 07/594,854
FILING DATE: 09-OCT-1990
APPLICATION NUMBER: US 07/594,854
FILING DATE: 20-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4600-0113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0860
TELEPHAX: 415-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-184-236-2
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181 YYLTRE 186
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 VICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDASGKRV 385
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                                                                       APPLICANT: Reyes, Gregory
APPLICANT: Kim, Jungsuh P.
APPLICANT: Kim, Jungsuh P.
APPLICANT: Meckli, Randolph
APPLICANT: Simonsen, Christian C.
TITLE OF INVENTION: Hepatitis C Virus Epitopes
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Peter J. Dehlinger
STREET: 350 Cambridge Ave., Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,410B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.9%; Score 884; DB 2; Best Local Similarity 87.6%; Pred. No. 2.2e-82; Matches 163; Conservative 11; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 505,611
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 594,854
FILING DATE: 09-OCT-1990
ATTORNEY,AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-076.21
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 22, 2005, 14:55:37
Job time : 44 secs
Sequence 2, Application US/08407410B
Patent No. 5843636
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 323-8302 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YYLTRE 186
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                                                                                                                                                                                                                                                                                                                                                   USA
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LENGTH: 580
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SEQ ID NO 4
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                                                                                      6; Search time 173 Seconds (without alignments) 1364.549 Million cell updates/sec
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Sequence 4, Ap
Sequence 107, A
Sequence 117, A
Sequence 109, A
Sequence 3, Ap
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Sequence 1, A
Sequence 1, A
Sequence 3, A
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                                                                                                                                                      3055
1 MASMSMSYTWTGALITPCAA......GGDIYHSLSRARPRHHHHH
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-211-455-1
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US-10-170-131-1
US-10-471-164-4
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                                                                                      September 22, 2005, 14:49:36
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB seq length: 585
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Sequence 110, App Sequence 106, App Sequence 82, Appl Sequence 82, Appl Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, Appl Sequence 54, Appl Sequence 54, Appl Sequence 64, Appl Sequence 64, Appl Sequence 92, Appl Sequence 160, App Sequence 160, Appl Sequence 160, Appl Sequence 160, Appl Sequence 89, Appl Sequence
US-09-921-397-110

US-09-921-397-1106

US-09-921-121A-82

US-09-899-082-82

US-09-899-046-214

US-09-899-046-214

US-09-899-044-82

US-09-851-138-54

US-09-851-138-54

US-09-851-138-62

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US-09-851-138-62

US-09-871-138-62

US-09-871-138-92

US-09-873-224-160

US-09-873-224-160

US-09-873-224-160

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US-09-899-044-89
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APPLICANT: Yagi, Yoshihiko
APPLICANT: Sheets, Michael P.
APPLICANT: Sheets, Michael P.
APPLICANT: Sheets, Michael P.
APPLICANT: Shelly, John A.
APPLICANT: Wells, Peter A.
APPLICANT: Belly, John A.
APPLICANT: Epps, Dennis E.
TITLE OF INVENTION: A Continuous-Read Assay for the Detection of De Novo HCV RNA Polyn TILLE OF INVENTION: A Activity
FILE REPERENCE: 02-333-A
CURRENT APPLICATION NUMBER: US/10/712,479
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: C-terminally truncated HCV NSSB polymerase (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 3055; DB 16; Length 580; Best Local Similarity 100.0%; Pred. No. 4.1e-269; Matches 580; Conservative 0; Mismatches 0; Indels 0;
Sequence 4, Application US/10712479
Publication No. US20040209283A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
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US-09-921-397-109 US-10-211-455-3 US-09-921-397-108 US-09-921-397-107 US-10-927-520-17

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                                                                                                                                                                                                                                                                                                                       ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG 484
                                                                                                                                                                                                                                                                                                                                                 421 ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFTLHSYSPG 480
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                                                                                                  241 QCCDLAPEARQAIRSLIERLYIGGPLINSKGQNCGYRRCRASGVLTTSCGNTLICYLKAT 300
                                                                                                                                                              364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
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                                                                               QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
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                 181 TLPQAVMGSSYGFQYSPKQRVEFLVNTWKSKKCPMGFSYDTRCFDSTVTESDIRVEESIY
                                                                                                                                                                                                                                                                  361 BLITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPINSWLGNIMYAPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SMSYTWTGALITPCAARESOLPINALSNSLVRHRNWVYSTTSRSAALROKKVTFDRLQVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKWALYDVVS
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                                                                                                                                                                                                                                             ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
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                                                                                                                                                              AACRAAKLODCTMLVNGDDLVVI CESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDL
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TITLE OF INVENTION: DIRECT BINDING ASSAY FOR IDENTIFYING
TITLE OF INVENTION: INHIBITORS OF HCV POLYMERASE
TITLE FOR INVENTION: INHIBITORS OF HCV POLYMERASE
CURRENT APPLICATION NUMBER: US/10/211,455
CURRENT APPLICATION NUMBER: 60/310,272
PRIOR FILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTERE OF WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRHHHHHH 580
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Best Local Similarity 95.5%; Pred. No. 2.9e-258;
Matches 552; Conservative 18; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/10211455; Publication No. US20030108862A1; GENERAL INFORMATION:
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LENGTH: 578
TYPE: PRT
ORGANISM: HCV
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US-10-211-455-1
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Publication No. US20050003348A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FALL REPERENCE:
TITLE OF INVENTION: Hepatits C Virus NS5B Polymerase Inhibitor Binding Pocket
FILE REFERENCE: 13/123
CURRENT FAPLICATION NUMBER: US/10/842,046
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/469,604
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
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LQVLDDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAV
                   LQVLDDHYRDVLKEMKAKASTVKAKLISVEEACKITPPHSAKSKFGYGAKDVRSLSSRAV
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ORGANISM: Hepatitis C virus
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Sequence 1, Application US/10170131

Sequence 1, Application US/10170131

Publication No. US20030171874A1

GENERAL INFORMATION:

APPLICANT: Leaburg, Charles A.

APPLICANT: Cable, Michael

APPLICANT: Mannarino, Anthony

APPLICANT: Mannarino, Anthony

TITLE OF INVENTION: Compositions of Hepatitis C Virus NS5B Polymerase and

TITLE OF INVENTION: Methods for Crystallizing Same

TITLE OF INVENTION: Methods for Crystallizing Same

TITLE SEFERNCE: 1NO98B US

CURRENT APPLICATION NUMBER: US/10/170,131

CURRENT PILING DATE: :2002-06-12

NUMBER OF SEQ ID NOS: 1

SOFTWARE PATENTY OF 1.
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9 SYTWIGALITPCAAEESKLPINALSNSLLRHHNWYYATTSRSAGLRQKKVTFDRLQVLDD
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NAME/KEY: VARIANT
LOCATION: (335)
OTHER INFORMATION: amino acids at 335, 344 and 550 may be threonine
OTHER INFORMATION: or valine at 335, valine or alanine at 344 and
CTHER INFORMATION: arginine or glutamine at 550
US-10-170-131-1
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LENGTH: 576
TYPE: PRT
ORGANISM: Hepatitis C virus
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                                 301 AACRAKKIQDCTMLVNGDDLVVICESAGTQEDAANLRVFTEAMTRYSAPPGDLPQPEYDL 360
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                                                                                                                                                   ARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPG
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                                                                        ELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLW
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Publication No US20040110126A1

GERREAL INFORMATION:

APPLICANT: GEOOFE KUKOLJ and Ginette MCKERCHER

TITLE OF INVENTION: HCV POLYMERASE INHIBITOR ASSAY

FILE REFERENCE: 13/094

CURRENT APPLICATION NUMBER: US/10/471,164

CURRENT PILING DATE: 2003-09-05

PRIOR APPLICATION NUMBER: 60/274,374

PRIOR APPLICATION NUMBER: 60/274,374

SEQ ID NO 3

LENGTH : Fast SEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 578

TYPE: RT
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                                                                                                                                                                                                                                                                                                                         18; Mismatches
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Matches 552, Conservative
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US-10-471-164-3
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LVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDASGK 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSKLPLAVMGSSYGFQYSFGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 AKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIRSVWKDLLEDTDIPIQTTIM
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  481 EINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAATCGKYLFNWAVRTKL----
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the hepatitis C virus and
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Sequence 17, Application US/10927520
Sequence 17, Application US/10927520
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: New HCV clade and prototype sequences thereof
CURRENT PAPLICATION NUMBER: US/10/927,520
CURRENT FILING DATE: 2004-08-27
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 17
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
45.5%; Score 1391; DB 9;
Best Local Similarity 87.7%; Pred. No. 7.4e-118;
Matches 263; Conservative 13; Mismatches 24;
                                                545 AASRLDLSGWFVAGYSGGDIYHSLSRARPRHHHHH
                                                                                                                                                                                                        SQUEGOTION APPLICATION US/09921397
FREENT NO. US20020151484A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SID nucleic acids and pol
TITLE OF INVENTION: Dathogenic strain of the
TITLE OF INVENTION: pathogenic strain of the
TITLE OF INVENTION: applications thereof
TITLE REFERENCE: B4809A - JAZ
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: EP 00402225.7
PRIOR APPLICATION NUMBER: EP 00402225.7
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver. 2.1
SCOTUD NO 107
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AACRAAKLODCTWLVNGDDLVVICESAGTQEDAANLRVFTEAMTRYSAPPGDLPQPEYDL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKAA 304
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                                                                                                                                         NRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKLKLFPIPAA
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369 ITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLWAR
                                            MILMTHPFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEI
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                                                                         MILMTHFFSILLAQEOLEKALDCOIYGACYSIEPLDLPOIIERLHGLSAFSLHSYSPGEI
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10471164
Publication No. US20040110126A1
GENERAL INFORMATION:
APPLICANT GEORGE KUKKLJ AND GINETE MCKERCHER
TITLE OF INVENTION: HCV POLYMERASE INHIBITOR ASSAY
FILE REFERENCE: 13/094
CURRENT APPLICATION NUMBER: US/10/471,164
CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/274,374
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.1%; Pred. No. 6.2e-240;
Matches 519; Conservative 19; Mismatches 7;
                                                                                                                                                                                                                                      SRLDLSGWFVAGYSGGDIYHSLSRARPR 574
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TYPE: PRT
ORGANISM: HCV
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APPLICANT: HYBRIGENICS

TITLE OF INVENTION: SID nucleic acids and polypeptides selected from TITLE OF INVENTION: pathogenic strain of the hepatitis C virus and TITLE OF INVENTION: applications thereof FILE REPERENCE: B4809A - JAZ

CURRENT PAPLICATION NUMBER: US/09/921,397

CURRENT PILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: EP 004402225.7

PRIOR PILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 156

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 109

LENGTH: 260 US-09-921-397-109 US-09-921-397-109 130 LLEDTDTPIQTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTLPQA 189 1 LLEDSVTPIDITIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSKLPLA 60 a ઠે

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CSSNVSVAHDASGKRVYYLT 389 CSSNVSVAHDGAGKRVYYLT 260

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122 HIRSVWKDLLEDTDTPI---QTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMA 178 176 YGQVAPDVVKAVMGDAYGF-VDPRTRVKRLLSMWSPD--AVGATCDTVCFDSTITPEDIM 232 359 OPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTVPLARAAWETARHTPVNSWLGNIIM 418 179 LYDVVSTLPQAVMGSSYGFQYSPKQRVEFLVNTWKAKKCPMGFSYDTRCFDSTVTENDIR 238 64 LDDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKF-GYGAKDVRSLSSR-AVN 121 1 MSMSYTWTD-VISFKTASKVLSATRAITSGFLKQRSLVYVTEPRDAELRKQKVTINRQPL 60 FPPSYHKQVRLAKEKASKVVGVMMDYDEVAAHTPSKSAKSHITGLRGTDVRSGAARKAVL CYLKAAAACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRVFTEAMTRYSAPPGDPP HSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYLFNWAVRTKL 4 MSMSYTWTGALITPCAABESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQV 419 YAPTUWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSL 239 VEESIYQCCDLAPEARQAIRSLTERLYVGGPMTNSKGQNCGYRRCRASGVLTTSCGNTLT 539 KLTPIPAASRLDLSGWFVAGYS------GGDIYHSLSR--ARPRHHHHH 580 Query Match
31.9%; Score 975.5; DB 14; Length 576;
Best Local Similarity 38.7%; Pred. No. 1.4e-79;
Matches 230; Conservative 93; Mismatches 236; Indels 35; US-110-211-455-3
; Sequence 3, Application US/10211455
; Sequence 3, Application US/10211455
; Publication No. US20030108862A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: INHIBITORS OF HCV POLYMERASE
; TITLE OF INVENTION: INHIBITORS OF HCV POLYMERASE
; FILE REFREENCE: 13/088
; CURRENT APPLICATION NUMBER: US/10/211,455
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310,272
; PRIOR PILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FRSENCE FOR WINDOWS VERSION 4.0 Matches 230; Conservative , ORGANISM: HCV US-10-211-455-3 SEQ ID NO 3 LENGTH: 576 TYPE: PRT 299 임 유 셤 ద 셤 쉱 ሯ 셤 ò 셤 ò 셤 ò ò ò ઠે ò

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Sequence 108, Application US/09921397 Patent No. US20020151484A1 GENERAL INFORMATION: US-09-921-397-108

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Query Match
Best Local Similarity 83.9%;
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
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121 ALNCEIY 127
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STATE: NEW YORK
COUNTRY: USA
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                                                                                    RESULT 13
US-09-921-397-106
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US-09-294-121A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 106
LENGTH: 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTLPQAVMGSSYGFQYSPKQRVEFLV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSKLPLAVMGSSYGFQYSFGQRVEFLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 VICESAGTOEDAASLRVFTEAMTRYSAPPGDPPOPEYDLELITSCSSNVSVAHDASGKRV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 YYLTRDPTVPLARAAWETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YYLTRDPTTPLARAAWETARHTPVNSWLGNIIMFAPTLWARMILMTHFPSVLIARDQLEQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VICESAGVQEDAASLRAFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDGAGKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 110, Application US/09921397

Patent No. US20020151484A1

GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
TITLE OF INVENTION: SID nucleic acids and polypeptides selected from a TITLE OF INVENTION: pathogenic strain of the hepatitis C virus and TITLE OF INVENTION: applications thereof
FILE REFERENCE: B4809A - JAZ
CURRENT APPLICATION NUMBER: US/09/921,397

CURRENT FILING DATE: 2001-08-02

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
  TITLE OF INVENTION: SID nucleic acids and polypeptides selected from TITLE OF INVENTION: SID nucleic acids and polypeptides crims and TITLE OF INVENTION: pathogenic strain of the hepatitis C virus and TITLE OF INVENTION: applications thereof FILE REFERENCE: 1480.94 - JAZ CURRENT APPLICATION NUMBER: US/09/921,397 CURRENT FILING DATE: 2001-08-02 PRIOR APPLICATION NUMBER: EP 00402225.7 PRIOR APPLICATION NUMBER: EP 00402225.7 RICH FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 156 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 108 LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 2.1e-48;
9; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                       30.0%; Score 915; DB 9; Length 199; 85.9%; Pred. No. 9.9e-75; Live 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 MINSKGONCGYRRCRASGV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.4%;
Best Local Similarity 89.8%;
Matches 114; Conservative 5
                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 110
LENGTH: 127
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-921-397-110
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69 RDVLKEMKAKASTVKAKLLSVEBACKLTPPHSAKSKFGYGAKDVRSLSSRAVNHIRSVWK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWIGALVIPCAAEEQKLPINALSNSLLRHHNLVYSTISRSACQRQKKVTFDRLQVLDSHY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 TWTGALITPCAAEESKLPINALSNSLLRHHNLVYSTTSRSASLRQKKVTFDRLQVLDDHY 68
                                                                                                         TITLE OF INVENTION: 51D nucleic acids and polypeptides selected from a TITLE OF INVENTION: pathogenic strain of the hepatitis C virus and TITLE OF INVENTION: applications thereof FILE REFERENCE: B4803A - JAZ CURRENT APPLICATION NUMBER: US/09/921,397
CURRENT FILING DATE: 2001-08-02
PRIOR PELING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 137;
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Fatent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUTVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO;
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
AMDRESSER: BIERMANN & MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 585; DB 9;
Pred. No. 6.9e-45;
7; Mismatches 15;
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APPLICATION NUMBER: 08/256,568
FILIGO DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 106, Application US/09921397
Patent No. US20020151484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 DLLEDTDTPIQTTIMAK 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 STVTENDIRVEESIYQCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 TISCGNTLICYLKAAAACRAAKLQDCTMLVNGDDLVVICESAGTQEDAASLRV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTSCGNTLTCYLKASAACRAAKLQDCTWLVCGDDLVVICESAGTQBDAASLRV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO TITLE OF INVENTION: PROCESS FOR TYPING OF HCV NUMBER OF SEQUENCES: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.7%; Score 570; DB 9; Best Local Similarity 95.6%; Pred. No. 1.2e-43; Matches 108; Conservative 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/899,082A
FILING DATE: 06-7ul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-7ul-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY AGENT INFORMATION:
NAME: CHARLES A. WUSERLIAN
REGISTRATION NUMBER: 19,683
FREFRENGE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8002
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERWAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82, Application US/09899082A Patent No. US20020106638A1 GENERAL INFORMATION:
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ZIP: 10016
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: be90
POSITION IN GENOME:
MAP POSITION: n85
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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US-09-899-082A-82
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## PRPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 37-NOV-1992

**PILING DATE: 37-NOV-1992

**ATTORNEY/AGENT INFORMATION:

**MARE: GARALES A. WISERLIAN

**REGISTRATION NUMBER: 19,683

**REFERENCE/DOCKET NUMBER: 410.004

**TELEPANT: (312) 661-8002

**INFORMATION INFORMATION:

**TELEPANT: (312) 661-8002

**INFORMATION SEQ 1D NO: 82: 8002

**SEQUENCE CHARACTERISTICS:

**SEQUENCE CHARACTERISTICS:

**SEQUENCE CHARACTERISTICS:

**SEQUENCE CHARACTERISTICS:

**SEQUENCE TYPE: amino acids

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